

SEQUENCE LISTING

<110> Teijin Pharma Limited
Komori, Toshihisa
Kanatani, Naoko
Yoshida, Carolina Andrea
Zanma, Akira
Kobayashi, Shinji
Yamana, Kei

<120> BONE AND/OR JOINT-DISEASE-ASSOCIATES GENES

<130> Q94468

<150> PCT/JP2004/015879

<151> 2004-10-20

<150> JP 2003-359172

<151> 2003-10-20

<160> 114

<170> PatentIn version 3.1

<210> 1
<211> 5220
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (274)...(1962)

<400> 1
cggaactgct tcgactgcaa agcttcaagc gcagcctggg agcggcctgg tggccctatc 60
ccggcagctc cacacagcag aacgcccctgg gtccctgaaa ctcgaaaccc gggctcagaa 120
ccagcggaaa ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgttgc 180
tgagagccgg gggacctgac cggagccag gccgcgtatg gcgcgcctt gatgtcacac 240
ggacgccagc gaggccagcg ctccggctgc agc atg gac cgc gcg ggg cgc ctg 294
Met Asp Arg Ala Gly Arg Leu
1 5

ggt gcg ggc ctg cgg gga ctc tgc gtg gct gca ctc gtg ctc gtg tgc 342
Gly Ala Gly Leu Arg Gly Leu Cys Val Ala Ala Leu Val Leu Val Cys
10 15 20

gcc gga cac ggg ggc cgc cgc gag gat ggg gga cca gct tgc tac gga 390
Ala Gly His Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly
25 30 35

gga ttc gac ctc tac ttc atc ctg gac aag tca gga agt gtg ctg cac 438
Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His
40 45 50 55

cac tgg aat gaa atc tac tac ttc gtg gag cag ttg gct cat aga ttc 486

His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe			
60	65	70	
atc agc cca cag cta agg atg tcc ttc att gtc ttc tct act cga ggg			534
Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly			
75	80	85	
aca act tta atg aaa cta act gag gac agg gaa cag atc cga caa ggc			582
Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly			
90	95	100	
cta gaa gag ctc cag aaa gtt ctg cca gga gga gac act tac atg cac			630
Leu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His			
105	110	115	
gaa gga ttc gag agg gcc agt gag cag att tac tat gag aac agt caa			678
Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Ser Gln			
120	125	130	135
gga tac agg acg gcg agc gtc atc atc gcg ttg acg gat ggg gag ctg			726
Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu			
140	145	150	
cac gag gac ctc ttc tac tca gag agg gag gct aac cga tcc cga			774
His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg			
155	160	165	
gac ctt ggt gcg att gtt tac tgc gtt ggc gtg aag gat ttc aat gaa			822
Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu			
170	175	180	
act cag ttg gct cgg att gca gac agt aag gac cac gtg ttt cct gtg			870
Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val			
185	190	195	
aac gac ggc ttc cag gct ctc caa ggc att atc cac tca att tta aag			918
Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys			
200	205	210	215
aaa tcc tgc atc gaa att ctg gcg gct gaa cca tcc acc atc tgc gcg			966
Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala			
220	225	230	
gga gag tcc ttt caa gtg gtc gta aga gga aat ggc ttc cga cat gcc			1014
Gly Glu Ser Phe Gln Val Val Arg Gly Asn Gly Phe Arg His Ala			
235	240	245	
cgc aat gtg gac agg gtc ctc tgc agc ttc aaa atc aat gac tca gtc			1062
Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val			
250	255	260	
acg ctc aat gag aag ccc ttt gct gtg gaa gac act tat ttg ctg tgc			1110
Thr Leu Asn Glu Lys Pro Phe Ala Val Glu Asp Thr Tyr Leu Leu Cys			
265	270	275	
cca gca cca atc ttg aaa gaa gtt ggc atg aaa gct gca ctg cag gtc			1158
Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val			
280	285	290	295
agc atg aac gac ggc ctg tcc atc tcc agt tct gtc atc atc acc			1206

Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr			
300	305	310	
acc aca cac tgt tca gac ggc tcc atc ctg gcg att gct ctg ctg gtc			1254
Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Val			
315	320	325	
ctc ttc ctg ctg gcc ctg gcg ctg ctc tgg tgg ttc tgg ccc ctc			1302
Leu Phe Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu			
330	335	340	
tgc tgc aca gtg atc atc aag gag gtc cct cca ccc cct gtt gag gag			1350
Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Val Glu Glu			
345	350	355	
agt gag gaa gaa gac gat gat ggt ttg cca aag aag aaa tgg ccc aca			1398
Ser Glu Glu Glu Asp Asp Gly Leu Pro Lys Lys Lys Trp Pro Thr			
360	365	370	375
gta gat gcc tct tat tat ggt gga cgc ggt gtg gga ggc att aaa aga			1446
Val Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly Ile Lys Arg			
380	385	390	
atg gag gtc cgc tgg gga gaa aag ggc tcc aca gaa gaa ggg gcg aag			1494
Met Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys			
395	400	405	
tta gaa aag gca aag aat gca cga gtc aag atg cca gag caa gaa tat			1542
Leu Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr			
410	415	420	
gag ttc cca gaa ccc cga aac ctc aac aac atg cgc cg ^g cct tcc			1590
Glu Phe Pro Glu Pro Arg Asn Leu Asn Asn Asn Met Arg Arg Pro Ser			
425	430	435	
tcg cct cgg aag tgg tac tcg ccc atc aag gga aaa ctc gat gcc ttg			1638
Ser Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu			
440	445	450	455
tgg gtt ctg ctg aga aaa gga tat gac cga gtg tct gtg atg agg cca			1686
Trp Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro			
460	465	470	
cag cca gga gac acg gga cgc tgt atc aac ttc acc aga gtg aag aac			1734
Gln Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn			
475	480	485	
agt cag cca gcc aag tat ccc ctg aac aac acc tac cac ccc agc tcc			1782
Ser Gln Pro Ala Lys Tyr Pro Leu Asn Asn Thr Tyr His Pro Ser Ser			
490	495	500	
cca cct ccc gct cct atc tac aca ccc cca ccc cct gct ccc cac tgc			1830
Pro Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Ala Pro His Cys			
505	510	515	
cct ccc cca gcc ccc agt gcc ccc act cct ccc att cct tcc cca cca			1878
Pro Pro Pro Ala Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro			
520	525	530	535
tcc act ctc ccc cct cct cag gcc cca ccc cct aac agg gca cct			1926

Ser	Thr	Leu	Pro	Pro	Pro	Pro	Gln	Ala	Pro	Pro	Pro	Asn	Arg	Ala	Pro	
																540
																545
																550
ccc	ccc	tcc	cga	cct	cct	cca	agg	cct	tct	gtc	tag	aacccaaagt				1972
Pro	Pro	Ser	Arg	Pro	Pro	Pro	Arg	Pro	Pro	Arg	Pro	Ser	Val			
																555
																560
ccgagctctg	ggctgcctga	gcaactccag	caggaggctt	ctctgctgaa	agaaaagatct											2032
gcccagccta	tgtggtgagt	ggcggctgat	gttgcacga	tttaaaagca	agtcgtgatg											2092
ggcagaacaa	aatgggcatt	ttgaactgcc	tgaagacaga	caatgagaca	ataacagtca											2152
cattatagcc	tgtgaccct	cacctctaga	ggaaggttcc	cgagatggcc	acattgccac											2212
agtgctctca	gccagattat	gtcccatgaa	gaccaggaag	aaagtgactt	ccaagaatgg											2272
aatgcagcat	tggataagaa	acacctggct	gagattctga	cctcaactgat	ttgactcttg											2332
attcttggac	tgggagccag	gccatctcca	cccctggtac	caccagcaa	ctctgaaaat											2392
gtgcagtgtc	cctagtatgc	atcgaatagg	tatccaactg	ggatctgcag	gttgccttat											2452
aaagagcata	tgctctattc	tctttccgaa	acttcctggt	ttcccagtga	tgagggaaagg											2512
ggaaaaggtgt	tgccatgctt	agaagttaga	ggacgtcagt	gctcagcact	gatggagaag											2572
cgttcatgggg	agtgtccagc	tcttacatct	agaaatggct	ggcttcagca	ggcacagttc											2632
ctaaaccaac	aagccttgtc	attgtcaaag	gcaacctact	aatgattcac	cttaaacatc											2692
aaggttgact	gtggcatagg	tcagagctga	tcacacagaa	cttccccat	gaaatcgcaa											2752
gttcctcat	cttcaaatac	ccaggacccc	agagattct	aaatccagct	aagagacagt											2812
agtcctgact	tggcaagaaa	accattccca	gttgtttac	tctgaaacag	gccgttgtat											2872
gtatggata	tctctccttg	gccttcaac	ctgctcacaa	gtattaccag	ttatgaagca											2932
aggagaaata	catccagtgt	gtaatagaaa	agctctgccc	acaatcccc	tgtcactcct											2992
ctacattatt	ctgaagctgc	ttggtcagtg	agccctttaa	cctcatgtag	actctggaca											3052
ctgtcaccca	atcatgaaaa	cagaggtcat	tgtcaaaggc	agtgtatagc	ctgtacaaaa											3112
atgatgcttc	ttcctcagt	ttccacaggc	ccaaaaattc	ctgtcttagg	ctcctaaacc											3172
tctaaacttt	ttcctggaac	aaaagatata	aaacgggcat	aagttttat	gttttggct											3232
gtgatctcca	aagatccttc	aagaactcaa	gttagcctca	ttcttccagc	ttgttttagaa											3292
cagaggcatc	caggtgtcat	gcactccata	gacaccaatc	cttgtcccc	aggcagacat											3352
tattaatcaa	tctcagcact	agttctaat	ttaatccaaat	tatattttc	cacagtactt											3412
cacatctctt	atgacctgtt	ggtcatcagt	tagaatttag	agagataaac	actgtttgta											3472
atccctacct	tagaaagaaa	agcagaggag	aatggggaa	ccaccagcat	aaaagttatt											3532
atctggggaa	aatcgacctg	aaagaacgcc	caagtccaag	acctatggtg	ctgacaccaa											3592

agtaaacactt	tcccaagtgt	accccagacc	ccactcttct	ccctgtggcc	accactccct	3652
gctttcagg	agttgtgaaa	aagatctcct	tcacccttac	tgtccccca	tattagaaca	3712
aggcttgtt	agtgttagtcc	ttgttaaaca	gggccagaa	tgtctcagcc	acctgagatg	3772
acattgctgg	gccccagaaa	accattccaa	ggagaatggg	ctccccaggc	tcagagcatg	3832
caactatgag	cccatggcaa	ctgtttgac	tgctggcagt	acaaaacggg	ccacccccaca	3892
ttacagctgc	aggatttg	cagccataag	aaagtatgaa	ccaagatgct	ggtgttgctg	3952
ttcaacaagc	atgggcttcg	gggaaggcag	cagactccga	gagcaggcct	tgtcagtgt	4012
cccaaggggc	tgtggtgaag	tgtctgagga	aaaatgaatg	ctgatacatg	gtgattctga	4072
gaagaatttg	caaggttga	ccttagaatt	tatggaatgt	cttccctgg	cattcagaat	4132
tatggctaga	agtttctaga	aaccgtcaag	gttaatacct	ttcagagtag	gtgattacag	4192
gcaggaagag	cttgatgtg	gtttacaaag	cccatcagtt	ctgtgtcatt	ccctgtaa	4252
aacaggagat	ggtgggtgtg	attagcaa	tgcattgtt	atttgg	ctccttggta	4312
ttgtccttac	ggaggatttt	ttttatataa	gccaat	ttgtatata	ttcatattcc	4372
acgtgacaga	tggaagcacg	tcctatcagt	gtgaataaaa	agaacagtt	tagaaatta	4432
ttaaagccag	tgatttcatg	gcaggttacc	ctaccaagct	gtgttgg	atctccatg	4492
accatactgc	ttttacaatg	tacaaatagt	tcctaggtga	cgagaccctc	ctttacataa	4552
tgccgatgac	agccttgctg	ggaactgcgg	tccttctgct	gtgacagcca	gctcgaaaac	4612
aggtcctgcc	tggagcttgc	cacacactt	aggagacat	aagagctgtc	tttccccagc	4672
gtcagggaca	aagctaccat	aaagaagtgg	aaaagtctt	gctctccagc	ctgggacaga	4732
ggtctctctg	gaacccaag	gaagagcaga	aatgatcctt	gcctgccact	gcacacaatg	4792
tgatggtgg	aaatccatca	aggaataatt	gtgagataat	gaccgacagt	tcaggcgcaa	4852
agggattca	tgctgtgtaa	agtgggtgg	attcg	aagctatgca	aagcctgatc	4912
ttactcacca	ggaggatgg	aagggtttt	ttagttatct	gagctcagct	gagttatcac	4972
gcttggagaa	ccgattaaa	ggaattagaa	tatgattct	gaatacacat	aacattaaac	5032
tcttctctt	ttctatggta	atttagttat	ggacg	ttattgttat	cg	5092
aaaagacttg	tcatcaccgc	actgtgtgt	aggagactgg	gctgaacctg	tacaatggta	5152
taccctggaa	gttgctttt	taaaaaaaaaa	taataataaa	cacctaaaat	caaaaaaaaaa	5212
aaaaaaaaa						5220

<210> 2
<211> 562

<212> PRT
<213> Mouse

<400> 2

Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys Val
1 5 10 15

Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg Glu Asp
20 25 30

Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
35 40 45

Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
50 55 60

Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
65 70 75 80

Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
85 90 95

Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
100 105 110

Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
115 120 125

Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
130 135 140

Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
145 150 155 160

Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
165 170 175

Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
180 185 190

Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
195 200 205

Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
210 215 220

Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
225 230 235 240

Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
245 250 255

Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
260 265 270

Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
275 280 285

Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
290 295 300

Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly Ser Ile
305 310 315 320

Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Leu Ala Leu Ala Leu
325 330 335

Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
340 345 350

Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Asp Asp Asp Gly Leu
355 360 365

Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
370 375 380

Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
385 390 395 400

Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val
405 410 415

Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
420 425 430

Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
435 440 445

Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
450 455 460

Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
465 470 475 480

Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
485 490 495

Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr Pro
500 505 510

Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
515 520 525

Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro Gln Ala
530 535 540

Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro Arg Pro
545 550 555 560

Ser Val

<210> 3
<211> 1734
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (257)..(1012)

<400> 3
cccacgcgtc cgcgcctcctg atctccagag gaccccgggc tggacaggg gccttggcga 60
ggctgcagct gctgtggcag tagcttggga tggaggtctt tcttgctggg aactgaggag 120
ctgagaggct cctgtcaggc tcctgtccta aactcttggc acttgcggtg gcttgggctt 180
cacacactgt cagacacatt cttggtgcc tcctcggcct caggttgaa gctggctcca 240
caagggacac ggtgac atg agg ggc aac cca ctg atc cat ctt ctg gcc att 292
Met Arg Gly Asn Pro Leu Ile His Leu Leu Ala Ile
1 5 10

tcc ttc ctc tgc att ctc tca atg gtg tat tcc cag ctg tgc cca gca 340
Ser Phe Leu Cys Ile Leu Ser Met Val Tyr Ser Gln Leu Cys Pro Ala
15 20 25

ccc tgt gcc tgt cct tgg aca cca ccc cag tgc cca ccg ggg gta ccc 388
Pro Cys Ala Cys Pro Trp Thr Pro Pro Gln Cys Pro Pro Gly Val Pro
30 35 40

ctg gtg ctg gat ggc tgt ggc tgc tgt cga gtg tgt gca cgg agg ctg Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu 45 50 55 60	436
ggg gag tcc tgc gac cac ctg cat gtc tgc gac ccc agc cag ggc ctg Gly Glu Ser Cys Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu 65 70 75	484
gtt tgt cag cct ggg gca ggc ccc agt ggc cgt ggt gct gtc tgc ctc Val Cys Gln Pro Gly Ala Gly Pro Ser Gly Arg Gly Ala Val Cys Leu 80 85 90	532
ttc gaa gag gat gac ggg agc tgt gag gtc aat ggc cgc agg tac ctg Phe Glu Glu Asp Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu 95 100 105	580
gat ggg gag acc ttt aaa ccc aat tgc agg gtt ttg tgc cgc tgt gat Asp Gly Glu Thr Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp 110 115 120	628
gac ggt ggt ttc acc tgc ctg ccg ctg tgc agt gag gat gtc cgg ctg Asp Gly Gly Phe Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu 125 130 135 140	676
ccc agc tgg gac tgc cca cgc ccc agg aga ata cag gtc cca gga agg Pro Ser Trp Asp Cys Pro Arg Pro Arg Arg Ile Gln Val Pro Gly Arg 145 150 155	724
tgc tgc ccc gag tgg gtc tgt gac cag gca gtc atg cag ccg gca atc Cys Cys Pro Glu Trp Val Cys Asp Gln Ala Val Met Gln Pro Ala Ile 160 165 170	772
cag ccc tcc tca gcc caa gga cac caa ctt tct gcc ctt gtc act cct Gln Pro Ser Ser Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro 175 180 185	820
gca tct gcc gat ggc ccc tgt cca aac tgg agc aca gcc tgg ggc ccc Ala Ser Ala Asp Gly Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro 190 195 200	868
tgc tca acc acc tgt ggg ttg ggc ata gcc acc cga gta tcc aac cag Cys Ser Thr Thr Cys Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln 205 210 215 220	916
aac cga ttc tgc caa ctg gag atc cag cgt cgc ctg tgt ctg tcc aga Asn Arg Phe Cys Gln Leu Glu Ile Gln Arg Arg Leu Cys Leu Ser Arg 225 230 235	964
ccc tgc ctg gca tcc agg agc cac ggc tca tgg aac agt gcc ttc tag Pro Cys Leu Ala Ser Arg Ser His Gly Ser Trp Asn Ser Ala Phe 240 245 250	1012
agccattgcg gggatgtgga tacagggcct gccattctca gcaaatgtcc ctaggaccag	1072
gccctggact gatggtagat gcccctctcc atgctttgg ctgcagttaa ctgtcctgg	1132
tggattcagt gtccagagcc tctgagcgat ccctgctctg tctgaggtgg gggaaagcagg	1192
tgaccagctc catttctctg gattctgacc caggcttctg gttctcctg gctagttcct	1252

caaaaacttcc ctgtatgaaa aggacaacca aaaggacctt taaagctaag ctgtactggg 1312
caagcctggc caccatgctg gggatagtga cagtaatagg taccaggcag cagattgcct 1372
gaaacatcca ggtcccttct tggacttcta tgtgcttgc ccaaagatta tgggtgacct 1432
tgtaagtgtg ccttcctga tctgagaaca ccctgcccgg ctgggaagaa ttttctggga 1492
acatgaagag atggaatcac actattctt aagcgttt ccaagtccag gaacttgacc 1552
tttgtatgg taaaaataca catctctta atgctcacaa agcaagaggc tccacacttc 1612
tggcaggcca gggccttct cttcagcatg agagagacaa ggaacagtag agtaccctcc 1672
tctggaggac tggcccggtc tggataaac acccaaatac agtgtggaaa aaaaaaaaaaa 1732
aa 1734

<210> 4
<211> 251
<212> PRT
<213> Mouse

<400> 4

Met Arg Gly Asn Pro Leu Ile His Leu Leu Ala Ile Ser Phe Leu Cys
1 5 10 15

Ile Leu Ser Met Val Tyr Ser Gln Leu Cys Pro Ala Pro Cys Ala Cys
20 25 30

Pro Trp Thr Pro Pro Gln Cys Pro Pro Gly Val Pro Leu Val Leu Asp
35 40 45

Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Ser Cys
50 55 60

Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu Val Cys Gln Pro
65 70 75 80

Gly Ala Gly Pro Ser Gly Arg Gly Ala Val Cys Leu Phe Glu Glu Asp
85 90 95

Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly Glu Thr
100 105 110

Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly Gly Phe
115 120 125

Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
130 135 140

Cys Pro Arg Pro Arg Arg Ile Gln Val Pro Gly Arg Cys Cys Pro Glu
145 150 155 160

Trp Val Cys Asp Gln Ala Val Met Gln Pro Ala Ile Gln Pro Ser Ser
165 170 175

Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala Asp
180 185 190

Gly Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr
195 200 205

Cys Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys
210 215 220

Gln Leu Glu Ile Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Leu Ala
225 230 235 240

Ser Arg Ser His Gly Ser Trp Asn Ser Ala Phe
245 250

<210> 5
<211> 3548
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (88)..(2190)

<400> 5
actggaccgc ccctcgaccc gggctgtgct ttgggtttct taagtctgtgc cgcgtgcgc 60

acggtagtga cgcgttttac ccggagc atg gcg gat acc ggc ttg cgc cgc gtg 114
Met Ala Asp Thr Gly Leu Arg Arg Val
1 5

gtt ccc agc gac ctt tat ccc ctt gtg ctc aga ttt ctg cgg gat agc 162
Val Pro Ser Asp Leu Tyr Pro Leu Val Leu Arg Phe Leu Arg Asp Ser
10 15 20 25

caa ctc tcg gag gtg gcc agt aaa ttt gca aaa gcg acc ggc gct aca 210
Gln Leu Ser Glu Val Ala Ser Lys Phe Ala Lys Ala Thr Gly Ala Thr
30 35 40

cag cag gac gcc aat gcc tcg tcc ctc ttg gac atc tat agc ttc tgg 258
Gln Gln Asp Ala Asn Ala Ser Ser Leu Leu Asp Ile Tyr Ser Phe Trp
45 50 55

ctc aag tcc acc aaa gcc cca aag gtg aag tta cag tca aat gga cca 306

Leu Lys Ser Thr Lys Ala Pro Lys Val Lys Leu Gln Ser Asn Gly Pro			
60	65	70	
gtg acc aag aag gct aag aaa gag act tca tcc agt gac agc agt gag			354
Val Thr Lys Lys Ala Lys Lys Glu Thr Ser Ser Ser Asp Ser Ser Glu			
75	80	85	
gac agc agt gag gac gag gac aaa aaa gcc cag gga ctt ccc aca cag			402
Asp Ser Ser Glu Asp Glu Asp Lys Lys Ala Gln Gly Leu Pro Thr Gln			
90	95	100	105
aag gct gcc gca cag gtc aag cga gcc agt gtg cct cag cat gct gga			450
Lys Ala Ala Ala Gln Val Lys Arg Ala Ser Val Pro Gln His Ala Gly			
110	115	120	
aag gca gca gcc aaa gct tca gag agc agc agt agt gaa gaa tcc agt			498
Lys Ala Ala Ala Lys Ala Ser Glu Ser Ser Ser Glu Glu Ser Ser			
125	130	135	
gag gaa gag gaa gag gac aaa aag aaa aag cct gtc cag aag gca gct			546
Glu Glu Glu Glu Asp Lys Lys Lys Pro Val Gln Lys Ala Ala			
140	145	150	
aag ccc caa gcc aag gca gtc aga cct cct gcg aag aag gca gag agc			594
Lys Pro Gln Ala Lys Ala Val Arg Pro Pro Ala Lys Lys Ala Glu Ser			
155	160	165	
tct gag tcg gac tca gac tcg gat tcg gac tcc agc tca gag gaa gaa			642
Ser Glu Ser Asp Ser Asp Ser Asp Ser Ser Ser Glu Glu Glu			
170	175	180	185
aca cca cag acc cag aag cca aag gca gct gtg gca gca aaa gct cag			690
Thr Pro Gln Thr Gln Lys Pro Lys Ala Ala Val Ala Ala Lys Ala Gln			
190	195	200	
act aaa gcc gaa gcc aaa cca ggt aca cca gcg aaa gca cag cct aag			738
Thr Lys Ala Glu Ala Lys Pro Gly Thr Pro Ala Lys Ala Gln Pro Lys			
205	210	215	
gta gcc aat ggc aaa gca gcc gcc agc agc agc agc agc agc agc agc			786
Val Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser			
220	225	230	
gat gac tca gag gaa gag aag aag gca gct gca cct ccc aag aag act			834
Asp Asp Ser Glu Glu Lys Lys Ala Ala Pro Pro Lys Lys Thr			
235	240	245	
gta cca aaa aag caa gtc gtg gcc aag gcc cca gtg aaa gta gct gcc			882
Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Val Ala Ala			
250	255	260	265
gcc ccc acc cag aag agc tcc agc agt gag gat tct tcc agt gaa gag			930
Ala Pro Thr Gln Lys Ser Ser Ser Glu Asp Ser Ser Glu Glu			
270	275	280	
gag gag gga cag aga caa ccc atg aag aaa aaa gca ggt ccc tac agt			978
Glu Glu Gly Gln Arg Gln Pro Met Lys Lys Lys Ala Gly Pro Tyr Ser			
285	290	295	
tca gtt cca cca ccc tct gtt cct tta cca aag aag tcc ccg gga acc			1026

Ser Val Pro Pro Pro Ser Val Pro Leu Pro Lys Lys Ser Pro Gly Thr			
300	305	310	
cag gct cca aag aaa gct gct gcg cag aca cag cct gca gac agc agt			1074
Gln Ala Pro Lys Lys Ala Ala Gln Thr Gln Pro Ala Asp Ser Ser			
315	320	325	
gac gac agc agt gac gat tct gat tca agt tct gag gaa gag aaa aaa			1122
Asp Asp Ser Ser Asp Asp Ser Ser Ser Glu Glu Glu Lys Lys			
330	335	340	345
cct cca gct aag acg gtc gtc tcc aag aca ccc gcc aaa gca gct cca			1170
Pro Pro Ala Lys Thr Val Val Ser Lys Thr Pro Ala Lys Ala Ala Pro			
350	355	360	
gtg aag aag aaa gca gaa agc tct tca gac agc tcg gat tct gac agt			1218
Val Lys Lys Ala Glu Ser Ser Asp Ser Ser Asp Ser Asp Ser Asp Ser			
365	370	375	
tct gag gat gaa gct cct gcc aag cca gtc agt aca acc aag agt ccc			1266
Ser Glu Asp Glu Ala Pro Ala Lys Pro Val Ser Thr Thr Lys Ser Pro			
380	385	390	
aag cca gct gtc act ccg aag cca tct gca gca aag gca gtg aca act			1314
Lys Pro Ala Val Thr Pro Lys Pro Ser Ala Ala Lys Ala Val Thr Thr			
395	400	405	
cct aag caa cct gca ggc agt aac cag aaa cct cag agc agg aag gct			1362
Pro Lys Gln Pro Ala Gly Ser Asn Gln Lys Pro Gln Ser Arg Lys Ala			
410	415	420	425
gac agc agc tcc agc gag gag gaa agc agc tcc agc gag gag gag gag			1410
Asp Ser Ser Ser Ser Glu Glu Ser Ser Ser Glu Glu Glu Glu Glu			
430	435	440	
gcc tcc aag aaa agt gcc aca acc ccc aag gcc aag gtg act gct aaa			1458
Ala Ser Lys Ser Ala Thr Thr Pro Lys Ala Lys Val Thr Ala Lys			
445	450	455	
gca gca ccc gcc aaa cag gcc cct cag gct gct ggg gac agc agc tct			1506
Ala Ala Pro Ala Lys Gln Ala Pro Gln Ala Ala Gly Asp Ser Ser Ser			
460	465	470	
gac tca gat agt tcc agc agt gaa gag gag gag aag act cct aag ccc			1554
Asp Ser Asp Ser Ser Ser Glu Glu Glu Glu Lys Thr Pro Lys Pro			
475	480	485	
cca gct aag aag aag gca gca ggt gga gcc gtt tct aca cca gcc cct			1602
Pro Ala Lys Lys Ala Ala Gly Gly Ala Val Ser Thr Pro Ala Pro			
490	495	500	505
ggg aag aaa gca gag gcc aag agc agc agc agc agc agc agc agc			1650
Gly Lys Lys Ala Glu Ala Lys Ser Ser Ser Ser Ser Ser Ser Ser			
510	515	520	
tcc gaa gat tcc agt gaa gag gag aaa aaa aag aag ccc aaa gct act			1698
Ser Glu Asp Ser Ser Glu Glu Lys Lys Lys Lys Pro Lys Ala Thr			
525	530	535	
acc cct aaa ata cag gca agc aag gcc aat ggc act cca gct tct ctg			1746

Thr Pro Lys Ile Gln Ala Ser Lys Ala Asn Gly Thr Pro Ala Ser Leu		
540	545	550
aat gga aaa gca gcc aag gaa agt gag gag gaa gag gag gag gaa gaa		1794
Asn Gly Lys Ala Ala Lys Glu Ser Glu Glu Glu Glu Glu Glu Glu		
555	560	565
aca gaa gag aag aaa aag gca gct ggg acc aag cca ggt tca ggc aaa		1842
Thr Glu Glu Lys Lys Ala Ala Gly Thr Lys Pro Gly Ser Gly Lys		
570	575	580
585		
aaa cgg aag cag aat gag acc gca gat gaa gca aca act cct caa gct		1890
Lys Arg Lys Gln Asn Glu Thr Ala Asp Glu Ala Thr Thr Pro Gln Ala		
590	595	600
aag aaa gtt aag ctc gag acc ccc aat acg ttt cca aaa agg aag aag		1938
Lys Lys Val Lys Leu Glu Thr Pro Asn Thr Phe Pro Lys Arg Lys Lys		
605	610	615
gga gaa aga agg gcg tct tcc cct ttc cga agg gtc agg gag gag gag		1986
Gly Glu Arg Arg Ala Ser Ser Pro Phe Arg Arg Val Arg Glu Glu Glu		
620	625	630
att gag gtg gac tct cga gtg gcg gac aat tcc ttt gat gcc aag cga		2034
Ile Glu Val Asp Ser Arg Val Ala Asp Asn Ser Phe Asp Ala Lys Arg		
635	640	645
ggt gca gct gga gac tgg ggg gag cga gcc aat cag gtt ctg aag ttc		2082
Gly Ala Ala Gly Asp Trp Gly Glu Arg Ala Asn Gln Val Leu Lys Phe		
650	655	660
665		
acc aaa ggc aag tcc ttc cgg cat gaa aaa acg aag aag aag cga ggc		2130
Thr Lys Gly Lys Ser Phe Arg His Glu Lys Thr Lys Lys Arg Gly		
670	675	680
agc tac cgg gga ggc tcc atc tct gtc cag gtc aat tcc gtc aaa ttc		2178
Ser Tyr Arg Gly Ser Ile Ser Val Gln Val Asn Ser Val Lys Phe		
685	690	695
gac agc gag tga cacgtggta tcctttggca aaggaagggt gattttggga		2230
Asp Ser Glu		
700		
gactggcact caactccagt ggacccagaa actccgtgtt aggagacagt tgtgacaagg		2290
acgggtgttga gcaggtcctg aggtgtgtca gcctgcagtc ctctcaggct cctttttctg		2350
gacagctgaa tatcaaggac aaaaaggatt tttttttta aagaaaccca ttcagttgtc		2410
aattgccttc ctgttctgtg ggtcttcata ctgagagatt tgtatattt atattaaatc		2470
atgtcataca gattttgtt gtgatttca gagatgactt ccacagatta aagtcttagc		2530
tgttgcttaa ggcaaagcaa aacaacacat ggtataatt ttccctactg gaggattctc		2590
tttatgtgaa agccctggtg ggcaatgaca taagtcttgt gatgattgtc tgctaagcat		2650
actctgtgct catcttcatc cattggcccc ggcaccaaag cttctagaag ccagcgtgga		2710
tctaccaact ttggggata aaattgccat tcttggtgca gtaacctact aattggcagg		2770

caggattctc gagtgtgtga atgccatgca gctgtctttg ttttgttctt ggttagctgtt	2830
actgctacat gtttacagta ctttttagttt taatttcgaa gtaagctttt ctgacagaca	2890
ttttgcaaca acttgactgt tgtatattga caagttcatg gatgtatttg attcttatta	2950
acatcaagga caggctggta agtacctgca tgggtgagtc actggtcaag gaaatggaga	3010
tgacctatga accctgggtgt gaagtagata cactggatct cctgggcacc tggagcagca	3070
gcaggagaca gccccaggag gcaggagggc tctaactaag caggaccatt ttgtcttcaa	3130
gtcggcacac aggagtaatt atgcccgtt caagttggtc ccctggactc actattagta	3190
ccttacctat aatgttactg atacagacta gccaggagggc agggaggcat agctgggtgg	3250
tagtgtgctt gcttagcatt catagaccaa gtgtgatctc tatcaccgca ggaagtaaag	3310
agcagagaga ttccctggcc aaggaggtgg attataaagc tgttaggatgt gaccattggc	3370
agtgagggca ggggtggac gtggctggcc tggtagaaaa cggataccgg gcattgcctc	3430
ccctgtttgg tgtccacgct cacctggtaa cctgctaaaa gctgtggcag ctccttgg	3490
aaggctgcat ggtcaaagtt ctgtgtctta ccacaaaaca ataaagtcaa tggttcct	3548

<210> 6
 <211> 700
 <212> PRT
 <213> Mouse

 <400> 6

Met Ala Asp Thr Gly Leu Arg Arg Val Val Pro Ser Asp Leu Tyr Pro
 1 5 10 15

Leu Val Leu Arg Phe Leu Arg Asp Ser Gln Leu Ser Glu Val Ala Ser
 20 25 30

Lys Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser
 35 40 45

Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Thr Lys Ala Pro
 50 55 60

Lys Val Lys Leu Gln Ser Asn Gly Pro Val Thr Lys Lys Ala Lys Lys
 65 70 75 80

Glu Thr Ser Ser Asp Ser Ser Glu Asp Ser Ser Glu Asp Glu Asp
 85 90 95

Lys Lys Ala Gln Gly Leu Pro Thr Gln Lys Ala Ala Ala Gln Val Lys

100

105

110

Arg Ala Ser Val Pro Gln His Ala Gly Lys Ala Ala Ala Lys Ala Ser
115 120 125

Glu Ser Ser Ser Ser Glu Glu Ser Ser Glu Glu Glu Glu Asp Lys
130 135 140

Lys Lys Lys Pro Val Gln Lys Ala Ala Lys Pro Gln Ala Lys Ala Val
145 150 155 160

Arg Pro Pro Ala Lys Lys Ala Glu Ser Ser Glu Ser Asp Ser Asp Ser
165 170 175

Asp Ser Asp Ser Ser Ser Glu Glu Thr Pro Gln Thr Gln Lys Pro
180 185 190

Lys Ala Ala Val Ala Ala Lys Ala Gln Thr Lys Ala Glu Ala Lys Pro
195 200 205

Gly Thr Pro Ala Lys Ala Gln Pro Lys Val Ala Asn Gly Lys Ala Ala
210 215 220

Ala Ser Ser Ser Ser Ser Ser Asp Asp Ser Glu Glu Glu Lys
225 230 235 240

Lys Ala Ala Ala Pro Pro Lys Lys Thr Val Pro Lys Lys Gln Val Val
245 250 255

Ala Lys Ala Pro Val Lys Val Ala Ala Ala Pro Thr Gln Lys Ser Ser
260 265 270

Ser Ser Glu Asp Ser Ser Glu Glu Glu Glu Gly Gln Arg Gln Pro
275 280 285

Met Lys Lys Lys Ala Gly Pro Tyr Ser Ser Val Pro Pro Pro Ser Val
290 295 300

Pro Leu Pro Lys Lys Ser Pro Gly Thr Gln Ala Pro Lys Lys Ala Ala
305 310 315 320

Ala Gln Thr Gln Pro Ala Asp Ser Ser Asp Asp Ser Ser Asp Asp Ser
325 330 335

Asp Ser Ser Ser Glu Glu Lys Lys Pro Pro Ala Lys Thr Val Val

340

345

350

Ser Lys Thr Pro Ala Lys Ala Ala Pro Val Lys Lys Lys Ala Glu Ser
355 360 365

Ser Ser Asp Ser Ser Asp Ser Asp Ser Ser Glu Asp Glu Ala Pro Ala
370 375 380

Lys Pro Val Ser Thr Thr Lys Ser Pro Lys Pro Ala Val Thr Pro Lys
385 390 395 400

Pro Ser Ala Ala Lys Ala Val Thr Thr Pro Lys Gln Pro Ala Gly Ser
405 410 415

Asn Gln Lys Pro Gln Ser Arg Lys Ala Asp Ser Ser Ser Glu Glu
420 425 430

Glu Ser Ser Ser Glu Glu Glu Ala Ser Lys Lys Ser Ala Thr
435 440 445

Thr Pro Lys Ala Lys Val Thr Ala Lys Ala Ala Pro Ala Lys Gln Ala
450 455 460

Pro Gln Ala Ala Gly Asp Ser Ser Ser Asp Ser Asp Ser Ser Ser Ser
465 470 475 480

Glu Glu Glu Lys Thr Pro Lys Pro Pro Ala Lys Lys Lys Ala Ala
485 490 495

Gly Gly Ala Val Ser Thr Pro Ala Pro Gly Lys Lys Ala Glu Ala Lys
500 505 510

Ser Ser Ser Ser Ser Ser Ser Ser Glu Asp Ser Ser Glu Glu
515 520 525

Glu Lys Lys Lys Pro Lys Ala Thr Thr Pro Lys Ile Gln Ala Ser
530 535 540

Lys Ala Asn Gly Thr Pro Ala Ser Leu Asn Gly Lys Ala Ala Lys Glu
545 550 555 560

Ser Glu Glu Glu Glu Glu Glu Thr Glu Glu Lys Lys Lys Ala
565 570 575

Ala Gly Thr Lys Pro Gly Ser Gly Lys Lys Arg Lys Gln Asn Glu Thr

580

585

590

Ala Asp Glu Ala Thr Thr Pro Gln Ala Lys Lys Val Lys Leu Glu Thr
 595 600 605

Pro Asn Thr Phe Pro Lys Arg Lys Lys Gly Glu Arg Arg Ala Ser Ser
 610 615 620

Pro Phe Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val
 625 630 635 640

Ala Asp Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly
 645 650 655

Glu Arg Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg
 660 665 670

His Glu Lys Thr Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile
 675 680 685

Ser Val Gln Val Asn Ser Val Lys Phe Asp Ser Glu
 690 695 700

<210> 7
 <211> 4126
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (16)..(4050)

<400> 7
 cgtgtttggc tcagc atg gcg gag atg aag agc cct acg aaa gct gag cct 51
 Met Ala Glu Met Lys Ser Pro Thr Lys Ala Glu Pro
 1 5 10

gcg act ccc gca gaa gcg gcg caa agc gac cgc cac agc ctg ctg gag 99
 Ala Thr Pro Ala Glu Ala Ala Gln Ser Asp Arg His Ser Leu Leu Glu
 15 20 25

cac agc cgc gag ttc ttg gac ttc tgg gac att gcg aaa ccg gat 147
 His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Asp
 30 35 40

cag gaa acg cgg ctc cgg gcc acg gag aag ttg ttg gag tac ttg cgc 195
 Gln Glu Thr Arg Leu Arg Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg
 45 50 55 60

aca agg ccc aat gat tcg gag atg aaa tat gcc ctg aag cgc cta atc 243
 Thr Arg Pro Asn Asp Ser Glu Met Lys Tyr Ala. Leu Lys Arg Leu Ile

	65	70	75	
act ggg ctt ggg gtg ggc cga gaa gcc gct acg gcc tgc tac agc ctg				291
Thr Gly Leu Gly Val Gly Arg Glu Ala Ala Thr Ala Cys Tyr Ser Leu				
80	85	90		
gcg ctg gca cag ctg ttg cag tct ttt gaa gac atc cca ttg tgt gac				339
Ala Leu Ala Gln Leu Leu Gln Ser Phe Glu Asp Ile Pro Leu Cys Asp				
95	100	105		
atc ctg gat cag ata caa gaa aaa tac agc cta caa gcc atg aac aag				387
Ile Leu Asp Gln Ile Gln Glu Lys Tyr Ser Leu Gln Ala Met Asn Lys				
110	115	120		
gca atg atg aga cct agt ctc ttt gca aac ctt ttt gga gtg cta gcc				435
Ala Met Met Arg Pro Ser Leu Phe Ala Asn Leu Phe Gly Val Leu Ala				
125	130	135	140	
ctc ttt cag tca ggc cgc cta gtg aag gac aaa gag gcc ctg atg aag				483
Leu Phe Gln Ser Gly Arg Leu Val Lys Asp Lys Glu Ala Leu Met Lys				
145	150	155		
tcc gtg caa ttg ctg aag atc ctg tcc caa cac ccc aac cac tta cag				531
Ser Val Gln Leu Leu Lys Ile Leu Ser Gln His Pro Asn His Leu Gln				
160	165	170		
gga cag cca ata aag gct ctg gtg gac atc ctc tct gag gtc cca gag				579
Gly Gln Pro Ile Lys Ala Leu Val Asp Ile Leu Ser Glu Val Pro Glu				
175	180	185		
tcc atg ttc cag gag atc ctg cca aag gtc ctc aag ggt aac atg aaa				627
Ser Met Phe Gln Glu Ile Leu Pro Lys Val Leu Lys Gly Asn Met Lys				
190	195	200		
gtg atc ctc cgc tct ccc aag tac ttg gag ctc ttc ctc ctg gct aag				675
Val Ile Leu Arg Ser Pro Lys Tyr Leu Glu Leu Phe Leu Ala Lys				
205	210	215	220	
cag agg gtg ccg aca aag ctc gag tca ctc atg ggc tcg gtt gac cta				723
Gln Arg Val Pro Thr Lys Leu Glu Ser Leu Met Gly Ser Val Asp Leu				
225	230	235		
ttc tca gaa gac aat att ccc agt ctg gtg aac atc ctg aag gtg gcc				771
Phe Ser Glu Asp Asn Ile Pro Ser Leu Val Asn Ile Leu Lys Val Ala				
240	245	250		
gcc aac tct gtc aag aag gag cac aag ctg cct aat gtg gct ctg gac				819
Ala Asn Ser Val Lys Lys Glu His Lys Leu Pro Asn Val Ala Leu Asp				
255	260	265		
ctg ctc cgc ctg gct ctc aag gag agc aga ttc gaa ctg ttc tgg aag				867
Leu Leu Arg Leu Ala Leu Lys Glu Ser Arg Phe Glu Leu Phe Trp Lys				
270	275	280		
aag gtt ttg gag gag ggg ctg ctg aag aat ccg tcc tgg aca tcc agc				915
Lys Val Leu Glu Glu Gly Leu Leu Lys Asn Pro Ser Trp Thr Ser Ser				
285	290	295	300	
tac atg tgc ttc cgc cta ctg ggt gcg tct ctg ccg ctt ctg tca gag				963
Tyr Met Cys Phe Arg Leu Leu Gly Ala Ser Leu Pro Leu Leu Ser Glu				

305	310	315	
gag cag ttg cag ttg gtg atg cga gga gac ttg atc cgc cat ttt ggg Glu Gln Leu Gln Leu Val Met Arg Gly Asp Leu Ile Arg His Phe Gly 320	325	330	1011
gag aac atg gtt att tct aag ccc caa aac cta ttt aag atc atc cca Glu Asn Met Val Ile Ser Lys Pro Gln Asn Leu Phe Lys Ile Ile Pro 335	340	345	1059
gag ata agt aca tac gtg ggt acc ttc cta gag ggg tgc cag gat gac Glu Ile Ser Thr Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp 350	355	360	1107
cct aag cgg cag ttg act atg gtg gcc ttt aca acc atc acc aat Pro Lys Arg Gln Leu Thr Met Met Val Ala Phe Thr Thr Ile Thr Asn 365	370	375	1155
caa ggt ctc cct gtc atg cct acc ttc tgg cgt gtc acg cgg ttt ttg Gln Gly Leu Pro Val Met Pro Thr Phe Trp Arg Val Thr Arg Phe Leu 385	390	395	1203
aat gct gaa gcc ctg cag agc tat gtg gcc tgg tgg cgg gac atg ttc Asn Ala Glu Ala Leu Gln Ser Tyr Val Ala Trp Leu Arg Asp Met Phe 400	405	410	1251
ctg cag cct gac ctg aac tcc ttg gtt gac ttc agc act gcc aac cag Leu Gln Pro Asp Leu Asn Ser Leu Val Asp Phe Ser Thr Ala Asn Gln 415	420	425	1299
aag aga gct cag gac gcc tcg ttg aat gtg cct gag cga gct gta ttc Lys Arg Ala Gln Asp Ala Ser Leu Asn Val Pro Glu Arg Ala Val Phe 430	435	440	1347
cgg ctc cgg aag tgg atc atc cac cgc ctg gtc agc ctt gtg gat cat Arg Leu Arg Lys Trp Ile Ile His Arg Leu Val Ser Leu Val Asp His 445	450	455	1395
ttg cat ctg gag aag gat gaa gct gtg gtt gag caa ata gcc agg ttt Leu His Leu Glu Lys Asp Glu Ala Val Val Glu Gln Ile Ala Arg Phe 465	470	475	1443
tgc ttg ttc cat gcc ttc ttt aag acg aag aag gct acg ccc cag atc Cys Leu Phe His Ala Phe Phe Lys Thr Lys Lys Ala Thr Pro Gln Ile 480	485	490	1491
cca gag acg aag cag cac ttc tcc ttc cct ttg gac gac cgc aac cgt Pro Glu Thr Lys Gln His Phe Ser Phe Pro Leu Asp Asp Arg Asn Arg 495	500	505	1539
ggg gtc ttt gtc agt gcc ttc agc cta ctg cag acg ctc agt gtg Gly Val Phe Val Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Val 510	515	520	1587
aag ttc agg cag aca cca gac ctg gct gaa aat ggg aag cct tgg act Lys Phe Arg Gln Thr Pro Asp Leu Ala Glu Asn Gly Lys Pro Trp Thr 525	530	535	1635
tac cgc ctg gtt cag ttg gca gac atg ctg ttg aac cat aac cgc aat Tyr Arg Leu Val Gln Leu Ala Asp Met Leu Leu Asn His Asn Arg Asn			1683

545	550	555	
gta acc agt gtg aca tcc ttg aca aca cag cag cgt cag gcc tgg gac Val Thr Ser Val Thr Ser Leu Thr Thr Gln Gln Arg Gln Ala Trp Asp 560	565	570	1731
cag atg atg agt act ctg aag gaa tta gag gcc cgc tcc tct gag acc Gln Met Met Ser Thr Leu Lys Glu Leu Glu Ala Arg Ser Ser Glu Thr 575	580	585	1779
agg gcc att gcc ttc cag cac ctg ctg ctt ctg gtg ggc ctc cac atc Arg Ala Ile Ala Phe Gln His Leu Leu Leu Val Gly Leu His Ile 590	595	600	1827
ttc aag tcc cct gca gaa agc tgt gat gtc cta gga gac att cag act Phe Lys Ser Pro Ala Glu Ser Cys Asp Val Leu Gly Asp Ile Gln Thr 605	610	615	1875
tgc atc aag aaa agc atg gag cag aat ccc cgc cga tca cgc tct aga Cys Ile Lys Lys Ser Met Glu Gln Asn Pro Arg Arg Ser Arg Ser Arg 625	630	635	1923
gcc aaa gcc tcc cag gag cca gta tgg gtg gag gtg atg gtg gag atc Ala Lys Ala Ser Gln Glu Pro Val Trp Val Glu Val Met Val Glu Ile 640	645	650	1971
ttg ctg tcc ttg ctg gct caa ccc agc aac ttg atg cgc cag gtg gtc Leu Leu Ser Leu Leu Ala Gln Pro Ser Asn Leu Met Arg Gln Val Val 655	660	665	2019
cgg agt gta ttt ggt cat atc tgt ccc cac ctt act cca cgt tgt ctg Arg Ser Val Phe Gly His Ile Cys Pro His Leu Thr Pro Arg Cys Leu 670	675	680	2067
cag cta atc ctg gct gtc ctc agc cct gtg aca aac gag gat gag gat Gln Leu Ile Leu Ala Val Leu Ser Pro Val Thr Asn Glu Asp Glu Asp 685	690	695	2115
gac aac gtg gtg gtc act gat gac gct gat gag aag cag ctg cag cat Asp Asn Val Val Val Thr Asp Asp Ala Asp Glu Lys Gln Leu Gln His 705	710	715	2163
gga gag gac gaa gac tca gat aat gag gac aat aag aac tca gag agt Gly Glu Asp Glu Asp Ser Asp Asn Glu Asp Asn Lys Asn Ser Glu Ser 720	725	730	2211
gac atg gac agt gag gat ggg gaa gaa agt gaa gag gag gac cgt gac Asp Met Asp Ser Glu Asp Gly Glu Glu Ser Glu Glu Glu Asp Arg Asp 735	740	745	2259
aaa gat gtg gac cca ggc ttc cgt caa cag ttg atg gaa gtg tta aaa Lys Asp Val Asp Pro Gly Phe Arg Gln Gln Leu Met Glu Val Leu Lys 750	755	760	2307
gct ggg aat gca ttg ggt gga gtg gac aac gag gag gag gag ctt Ala Gly Asn Ala Leu Gly Gly Val Asp Asn Glu Glu Glu Glu Leu 765	770	775	2355
ggg gat gag gcc atg atg gcc ctg gac cag aac ctg gcc agc cta ttt Gly Asp Glu Ala Met Met Ala Leu Asp Gln Asn Leu Ala Ser Leu Phe			2403

785	790	795	
aaa gag cag aag atg cgc atc cag gcc cg	aat gag gag aaa aac aag		2451
Lys Glu Gln Lys Met Arg Ile Gln Ala Arg Asn Glu Glu Lys Asn Lys			
800	805	810	
ctc cag aag gag aag aag ctc cga cgg gac ttc caa atc agg gca cta			2499
Leu Gln Lys Glu Lys Lys Leu Arg Arg Asp Phe Gln Ile Arg Ala Leu			
815	820	825	
gac ctg atc gag gtg ctg gtg acc aag cag cct gag cac ccc ctg atc			2547
Asp Leu Ile Glu Val Leu Val Thr Lys Gln Pro Glu His Pro Leu Ile			
830	835	840	
ctg gaa cta ctt gag cca ctg ctg aac gtg atc cag cac agc atg cgc			2595
Leu Glu Leu Leu Glu Pro Leu Leu Asn Val Ile Gln His Ser Met Arg			
845	850	855	860
agc aaa ggc tcc acc aag cag gag cag gac ctc ctg cac aag acc gcc			2643
Ser Lys Gly Ser Thr Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala			
865	870	875	
cgc atc ttc atg cac cac ctg tgt cgt gcc cgc cgc tac tgc cac gag			2691
Arg Ile Phe Met His His Leu Cys Arg Ala Arg Arg Tyr Cys His Glu			
880	885	890	
gtg ggg ccg tgt gca gag gct ctg cat gcc cag gtg gag agg ctt gtg			2739
Val Gly Pro Cys Ala Glu Ala Leu His Ala Gln Val Glu Arg Leu Val			
895	900	905	
cag cag gct ggc agc cag gct gat gcc tct gtc gcc cta tac tat ttc			2787
Gln Gln Ala Gly Ser Gln Ala Asp Ala Ser Val Ala Leu Tyr Tyr Phe			
910	915	920	
aat gcc tct ctg tac ctg ctg cga gtc ctc aag ggc aac acc aat aag			2835
Asn Ala Ser Leu Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Asn Lys			
925	930	935	940
agg cac caa gat ggt cat aag tta cac gga gct gac aca gag gac tca			2883
Arg His Gln Asp Gly His Lys Leu His Gly Ala Asp Thr Glu Asp Ser			
945	950	955	
gag gac cag gct aac tgc tta gac ttg gac ttt gtg acc cgg gtg			2931
Glu Asp Gln Ala Ala Asn Cys Leu Asp Leu Asp Phe Val Thr Arg Val			
960	965	970	
tat tca gca tca ctg gaa tct ctt ctg acc aag cgt aac agc tca ctt			2979
Tyr Ser Ala Ser Leu Glu Ser Leu Leu Thr Lys Arg Asn Ser Ser Leu			
975	980	985	
acg gtc ccc atg ttc ctc agc ctc ttc tcc aga tac cca gtg atc tgt			3027
Thr Val Pro Met Phe Leu Ser Leu Phe Ser Arg Tyr Pro Val Ile Cys			
990	995	1000	
aag aac ctg ctt ccc gtc ctg gct cag cat gtg gct ggc cca tct			3072
Lys Asn Leu Leu Pro Val Leu Ala Gln His Val Ala Gly Pro Ser			
1005	1010	1015	
cgg ccc cgc cat cag gcc cag gca tgc ctg atg ctc cag aag act			3117
Arg Pro Arg His Gln Ala Gln Ala Cys Leu Met Leu Gln Lys Thr			

1020	1025	1030	
ctg tct gca cga gag ctg	aga gtc tgt ttt gag	gat cct gag tgg	3162
Leu Ser Ala Arg Glu Leu	Arg Val Cys Phe Glu	Asp Pro Glu Trp	
1035 1040	1045		
gag cag ctg att acccaa	ctc ttg gga aag gcc	acc cag acc ctg	3207
Glu Gln Leu Ile Thr Gln	Leu Leu Gly Lys Ala	Thr Gln Thr Leu	
1050 1055	1060		
cag act ctt ggg gag gca	cag agc aag ggg gag	cac cag aag gag	3252
Gln Thr Leu Gly Glu Ala	Gln Ser Lys Gly Glu	His Gln Lys Glu	
1065 1070	1075		
cta tcc atc ttg gag ctg	ctg aac act ctg ttg	agg aca gtc aat	3297
Leu Ser Ile Leu Glu Leu	Leu Asn Thr Leu Leu	Arg Thr Val Asn	
1080 1085	1090		
cac gag aag ctg tct gtg	gac ctc act gct ccc	ttg ggc gtg ctt	3342
His Glu Lys Leu Ser Val	Asp Leu Thr Ala Pro	Leu Gly Val Leu	
1095 1100	1105		
cag agc aag caa cag aag	ctg cag caa agc ctg	cag cag ggg aat	3387
Gln Ser Lys Gln Gln Lys	Leu Gln Gln Ser Leu	Gln Gln Gly Asn	
1110 1115	1120		
cac tca tct ggc tcc aat	cgc ctc tat gat ctc	tac tgg cag gcc	3432
His Ser Ser Gly Ser Asn	Arg Leu Tyr Asp Leu	Tyr Trp Gln Ala	
1125 1130	1135		
atg agg atg cta gga gtc	caa cgt cca aag tca	gaa aag aag aat	3477
Met Arg Met Leu Gly Val	Gln Arg Pro Lys Ser	Glu Lys Lys Asn	
1140 1145	1150		
gcc aag gat att cct agt	gac acc cag agc ccc	gtc agc aca aag	3522
Ala Lys Asp Ile Pro Ser	Asp Thr Gln Ser Pro	Val Ser Thr Lys	
1155 1160	1165		
cgg aag aaa aag gga ttc	ttg cca gag acc aag	aag cga aag aaa	3567
Arg Lys Lys Lys Gly Phe	Leu Pro Glu Thr Lys	Lys Arg Lys Lys	
1170 1175	1180		
ctt aaa tct gag ggc acc	aca cca gaa aag aat	gct gcg tca cag	3612
Leu Lys Ser Glu Gly Thr	Thr Pro Glu Lys Asn	Ala Ala Ser Gln	
1185 1190	1195		
cag gat gca gtg aca gag	ggt gcc atg cct gct	gcc act ggt aaa	3657
Gln Asp Ala Val Thr Glu	Gly Ala Met Pro Ala	Ala Thr Gly Lys	
1200 1205	1210		
gac cag ccc ccc agc aca	ggc aag aag aaa agg	aag agg gta aag	3702
Asp Gln Pro Pro Ser Thr	Gly Lys Lys Lys Arg	Lys Arg Val Lys	
1215 1220	1225		
gcc agc acc cca tcc cag	gtg aat ggg ata act	ggg gcc aag agt	3747
Ala Ser Thr Pro Ser Gln	Val Asn Gly Ile Thr	Gly Ala Lys Ser	
1230 1235	1240		
cca gct ccc agt aac ccc	acc cta agc ccc agc	acc cct gcc aag	3792
Pro Ala Pro Ser Asn Pro	Thr Leu Ser Pro Ser	Thr Pro Ala Lys	

1245	1250	1255	
acc cca aaa ctg cag aag aaa aaa gag aag ctg tca cag gtg aat			3837
Thr Pro Lys Leu Gln Lys Lys Lys Glu Lys Leu Ser Gln Val Asn			
1260	1265	1270	
gga gcc act cct gtg tcc ccc ata gag cct gaa agc aaa aag cat			3882
Gly Ala Thr Pro Val Ser Pro Ile Glu Pro Glu Ser Lys Lys His			
1275	1280	1285	
cat cag gag gca ctc agc aca aag gag gtc ata aga aag tcc ccc			3927
His Gln Glu Ala Leu Ser Thr Lys Glu Val Ile Arg Lys Ser Pro			
1290	1295	1300	
cac ccc cag tct gcc ctg cca aag aaa aga gca agg ctg tct ctg			3972
His Pro Gln Ser Ala Leu Pro Lys Lys Arg Ala Arg Leu Ser Leu			
1305	1310	1315	
gtg agc agg agc ccc agc ctg tta cag agt ggg gtc aag aaa agg			4017
Val Ser Arg Ser Pro Ser Leu Leu Gln Ser Gly Val Lys Lys Arg			
1320	1325	1330	
aga gtg gcc agc agg aga gtg cag aca cct tga gtgtgtatag			4060
Arg Val Ala Ser Arg Arg Val Gln Thr Pro			
1335	1340		
tctgtttccc tgccctagag actcctatTT tttcaccaat attttaataa acaatccatg			4120
atgcta			4126

<210> 8
 <211> 1344
 <212> PRT
 <213> Mouse

<400> 8

Met Ala Glu Met Lys Ser Pro Thr Lys Ala Glu Pro Ala Thr Pro Ala			
1	5	10	15

Glu Ala Ala Gln Ser Asp Arg His Ser Leu Leu Glu His Ser Arg Glu		
20	25	30

Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Asp Gln Glu Thr Arg		
35	40	45

Leu Arg Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Thr Arg Pro Asn		
50	55	60

Asp Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly Leu Gly			
65	70	75	80

Val Gly Arg Glu Ala Ala Thr Ala Cys Tyr Ser Leu Ala Leu Ala Gln		
85	90	95

Leu Leu Gln Ser Phe Glu Asp Ile Pro Leu Cys Asp Ile Leu Asp Gln
100 105 110

Ile Gln Glu Lys Tyr Ser Leu Gln Ala Met Asn Lys Ala Met Met Arg
115 120 125

Pro Ser Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe Gln Ser
130 135 140

Gly Arg Leu Val Lys Asp Lys Glu Ala Leu Met Lys Ser Val Gln Leu
145 150 155 160

Leu Lys Ile Leu Ser Gln His Pro Asn His Leu Gln Gly Gln Pro Ile
165 170 175

Lys Ala Leu Val Asp Ile Leu Ser Glu Val Pro Glu Ser Met Phe Gln
180 185 190

Glu Ile Leu Pro Lys Val Leu Lys Gly Asn Met Lys Val Ile Leu Arg
195 200 205

Ser Pro Lys Tyr Leu Glu Leu Phe Leu Leu Ala Lys Gln Arg Val Pro
210 215 220

Thr Lys Leu Glu Ser Leu Met Gly Ser Val Asp Leu Phe Ser Glu Asp
225 230 235 240

Asn Ile Pro Ser Leu Val Asn Ile Leu Lys Val Ala Ala Asn Ser Val
245 250 255

Lys Lys Glu His Lys Leu Pro Asn Val Ala Leu Asp Leu Leu Arg Leu
260 265 270

Ala Leu Lys Glu Ser Arg Phe Glu Leu Phe Trp Lys Lys Val Leu Glu
275 280 285

Glu Gly Leu Leu Lys Asn Pro Ser Trp Thr Ser Ser Tyr Met Cys Phe
290 295 300

Arg Leu Leu Gly Ala Ser Leu Pro Leu Leu Ser Glu Glu Gln Leu Gln
305 310 315 320

Leu Val Met Arg Gly Asp Leu Ile Arg His Phe Gly Glu Asn Met Val
325 330 335

Ile Ser Lys Pro Gln Asn Leu Phe Lys Ile Ile Pro Glu Ile Ser Thr
340 345 350

Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Lys Arg Gln
355 360 365

Leu Thr Met Met Val Ala Phe Thr Thr Ile Thr Asn Gln Gly Leu Pro
370 375 380

Val Met Pro Thr Phe Trp Arg Val Thr Arg Phe Leu Asn Ala Glu Ala
385 390 395 400

Leu Gln Ser Tyr Val Ala Trp Leu Arg Asp Met Phe Leu Gln Pro Asp
405 410 415

Leu Asn Ser Leu Val Asp Phe Ser Thr Ala Asn Gln Lys Arg Ala Gln
420 425 430

Asp Ala Ser Leu Asn Val Pro Glu Arg Ala Val Phe Arg Leu Arg Lys
435 440 445

Trp Ile Ile His Arg Leu Val Ser Leu Val Asp His Leu His Leu Glu
450 455 460

Lys Asp Glu Ala Val Val Glu Gln Ile Ala Arg Phe Cys Leu Phe His
465 470 475 480

Ala Phe Phe Lys Thr Lys Ala Thr Pro Gln Ile Pro Glu Thr Lys
485 490 495

Gln His Phe Ser Phe Pro Leu Asp Asp Arg Asn Arg Gly Val Phe Val
500 505 510

Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Val Lys Phe Arg Gln
515 520 525

Thr Pro Asp Leu Ala Glu Asn Gly Lys Pro Trp Thr Tyr Arg Leu Val
530 535 540

Gln Leu Ala Asp Met Leu Leu Asn His Asn Arg Asn Val Thr Ser Val
545 550 555 560

Thr Ser Leu Thr Thr Gln Gln Arg Gln Ala Trp Asp Gln Met Met Ser
565 570 575

Thr Leu Lys Glu Leu Glu Ala Arg Ser Ser Glu Thr Arg Ala Ile Ala
580 585 590

Phe Gln His Leu Leu Leu Val Gly Leu His Ile Phe Lys Ser Pro
595 600 605

Ala Glu Ser Cys Asp Val Leu Gly Asp Ile Gln Thr Cys Ile Lys Lys
610 615 620

Ser Met Glu Gln Asn Pro Arg Arg Ser Arg Ser Arg Ala Lys Ala Ser
625 630 635 640

Gln Glu Pro Val Trp Val Glu Val Met Val Glu Ile Leu Leu Ser Leu
645 650 655

Leu Ala Gln Pro Ser Asn Leu Met Arg Gln Val Val Arg Ser Val Phe
660 665 670

Gly His Ile Cys Pro His Leu Thr Pro Arg Cys Leu Gln Leu Ile Leu
675 680 685

Ala Val Leu Ser Pro Val Thr Asn Glu Asp Glu Asp Asp Asn Val Val
690 695 700

Val Thr Asp Asp Ala Asp Glu Lys Gln Leu Gln His Gly Glu Asp Glu
705 710 715 720

Asp Ser Asp Asn Glu Asp Asn Lys Asn Ser Glu Ser Asp Met Asp Ser
725 730 735

Glu Asp Gly Glu Glu Ser Glu Glu Asp Arg Asp Lys Asp Val Asp
740 745 750

Pro Gly Phe Arg Gln Gln Leu Met Glu Val Leu Lys Ala Gly Asn Ala
755 760 765

Leu Gly Gly Val Asp Asn Glu Glu Glu Glu Leu Gly Asp Glu Ala
770 775 780

Met Met Ala Leu Asp Gln Asn Leu Ala Ser Leu Phe Lys Glu Gln Lys
785 790 795 800

Met Arg Ile Gln Ala Arg Asn Glu Glu Lys Asn Lys Leu Gln Lys Glu
805 810 815

Lys Lys Leu Arg Arg Asp Phe Gln Ile Arg Ala Leu Asp Leu Ile Glu
820 825 830

Val Leu Val Thr Lys Gln Pro Glu His Pro Leu Ile Leu Glu Leu Leu
835 840 845

Glu Pro Leu Leu Asn Val Ile Gln His Ser Met Arg Ser Lys Gly Ser
850 855 860

Thr Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala Arg Ile Phe Met
865 870 875 880

His His Leu Cys Arg Ala Arg Arg Tyr Cys His Glu Val Gly Pro Cys
885 890 895

Ala Glu Ala Leu His Ala Gln Val Glu Arg Leu Val Gln Gln Ala Gly
900 905 910

Ser Gln Ala Asp Ala Ser Val Ala Leu Tyr Tyr Phe Asn Ala Ser Leu
915 920 925

Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Asn Lys Arg His Gln Asp
930 935 940

Gly His Lys Leu His Gly Ala Asp Thr Glu Asp Ser Glu Asp Gln Ala
945 950 955 960

Ala Asn Cys Leu Asp Leu Asp Phe Val Thr Arg Val Tyr Ser Ala Ser
965 970 975

Leu Glu Ser Leu Leu Thr Lys Arg Asn Ser Ser Leu Thr Val Pro Met
980 985 990

Phe Leu Ser Leu Phe Ser Arg Tyr Pro Val Ile Cys Lys Asn Leu Leu
995 1000 1005

Pro Val Leu Ala Gln His Val Ala Gly Pro Ser Arg Pro Arg His
1010 1015 1020

Gln Ala Gln Ala Cys Leu Met Leu Gln Lys Thr Leu Ser Ala Arg
1025 1030 1035

Glu Leu Arg Val Cys Phe Glu Asp Pro Glu Trp Glu Gln Leu Ile
1040 1045 1050

Thr Gln Leu Leu Gly Lys Ala Thr Gln Thr Leu Gln Thr Leu Gly
1055 1060 1065

Glu Ala Gln Ser Lys Gly Glu His Gln Lys Glu Leu Ser Ile Leu
1070 1075 1080

Glu Leu Leu Asn Thr Leu Leu Arg Thr Val Asn His Glu Lys Leu
1085 1090 1095

Ser Val Asp Leu Thr Ala Pro Leu Gly Val Leu Gln Ser Lys Gln
1100 1105 1110

Gln Lys Leu Gln Gln Ser Leu Gln Gln Gly Asn His Ser Ser Gly
1115 1120 1125

Ser Asn Arg Leu Tyr Asp Leu Tyr Trp Gln Ala Met Arg Met Leu
1130 1135 1140

Gly Val Gln Arg Pro Lys Ser Glu Lys Lys Asn Ala Lys Asp Ile
1145 1150 1155

Pro Ser Asp Thr Gln Ser Pro Val Ser Thr Lys Arg Lys Lys Lys
1160 1165 1170

Gly Phe Leu Pro Glu Thr Lys Lys Arg Lys Lys Leu Lys Ser Glu
1175 1180 1185

Gly Thr Thr Pro Glu Lys Asn Ala Ala Ser Gln Gln Asp Ala Val
1190 1195 1200

Thr Glu Gly Ala Met Pro Ala Ala Thr Gly Lys Asp Gln Pro Pro
1205 1210 1215

Ser Thr Gly Lys Lys Lys Arg Lys Arg Val Lys Ala Ser Thr Pro
1220 1225 1230

Ser Gln Val Asn Gly Ile Thr Gly Ala Lys Ser Pro Ala Pro Ser
1235 1240 1245

Asn Pro Thr Leu Ser Pro Ser Thr Pro Ala Lys Thr Pro Lys Leu
1250 1255 1260

Gln Lys Lys Lys Glu Lys Leu Ser Gln Val Asn Gly Ala Thr Pro
1265 1270 1275

Val Ser Pro Ile Glu Pro Glu Ser Lys Lys His His Gln Glu Ala
1280 1285 1290

Leu Ser Thr Lys Glu Val Ile Arg Lys Ser Pro His Pro Gln Ser
1295 1300 1305

Ala Leu Pro Lys Lys Arg Ala Arg Leu Ser Leu Val Ser Arg Ser
1310 1315 1320

Pro Ser Leu Leu Gln Ser Gly Val Lys Lys Arg Arg Val Ala Ser
1325 1330 1335

Arg Arg Val Gln Thr Pro
1340

<210> 9
<211> 2851
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (76) .. (2349)

<400> 9
acgcgggggg aagtgcagcg tgcgtgcgtt ttgggtggtc gctgtgtgcg ctccgcgtgt 60
gcagccgcgt gggcc atg ggg cgg cgg gcg cgg ggc cgg cgg ttc cag cag 111
Met Gly Arg Arg Ala Arg Gly Arg Arg Phe Gln Gln
1 5 10
ccg ccg cct gag ggc gag gaa gac gcc agc gac ggc ggc aga aag 159
Pro Pro Gln Pro Glu Gly Glu Asp Ala Ser Asp Gly Gly Arg Lys
15 20 25
cga ggc cag gcg ggc tgg gaa ggt ggc tat ccc gag atc gta aag gag 207
Arg Gly Gln Ala Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu
30 35 40
aac aag ctc ttc gag cac tac tat cag gaa ctc aag atc gtg cca gag 255
Asn Lys Leu Phe Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu
45 50 55 60
gga gaa tgg gac caa ttc atg gag tca ctc cga gaa cct ctc cca gcc 303
Gly Glu Trp Asp Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala
65 70 75
aca ctg aga atc act ggg tac aaa agc cat gcc aaa gag att ctc cat 351
Thr Leu Arg Ile Thr Gly Tyr Lys Ser His Ala Lys Glu Ile Leu His
80 85 90
tgc ttg aag aac aag tac ttt aag gag ttg gag gac ctg gaa gta gat 399

Cys	Leu	Lys	Asn	Lys	Tyr	Phe	Lys	Glu	Leu	Glu	Asp	Leu	Glu	Val	Asp	
95							100					105				
gga	cag	aaa	gtt	gaa	gtt	cca	caa	cca	cta	agc	tgg	tac	cct	gaa	gaa	447
Gly	Gln	Lys	Val	Glu	Val	Pro	Gln	Pro	Leu	Ser	Trp	Tyr	Pro	Glu	Glu	
110						115					120					
ctt	gcc	tgg	cat	aca	aac	tta	agt	cgg	aaa	atc	ttg	agg	aag	tcc	ccg	495
Leu	Ala	Trp	His	Thr	Asn	Leu	Ser	Arg	Lys	Ile	Leu	Arg	Lys	Ser	Pro	
125						130				135				140		
ttg	ttg	gca	aag	ttc	cat	cag	ttc	ctg	gtc	agc	gag	act	gag	tct	gga	543
Leu	Leu	Ala	Lys	Phe	His	Gln	Phe	Leu	Val	Ser	Glu	Thr	Glu	Ser	Gly	
145						150				155						
aac	atc	agc	cgc	cag	gag	gct	gtc	agc	atg	atc	ccc	cca	ctg	ctg	ctc	591
Asn	Ile	Ser	Arg	Gln	Glu	Ala	Val	Ser	Met	Ile	Pro	Pro	Leu	Leu		
160						165				170						
aac	gtg	gag	cca	cac	cat	aag	atc	tta	gac	atg	tgt	gca	gcc	cct	gga	639
Asn	Val	Glu	Pro	His	His	Lys	Ile	Leu	Asp	Met	Cys	Ala	Ala	Pro	Gly	
175						180				185						
tcc	aag	acc	aca	cag	tta	att	gaa	atg	ttg	cat	gca	gac	atg	agt	gtg	687
Ser	Lys	Thr	Thr	Gln	Leu	Ile	Glu	Met	Leu	His	Ala	Asp	Met	Ser	Val	
190						195				200						
ccc	ttt	cca	gag	gga	ttt	gta	atc	gca	aat	gac	gtg	gac	aac	aag	cgc	735
Pro	Phe	Pro	Glu	Gly	Phe	Val	Ile	Ala	Asn	Asp	Val	Asp	Asn	Lys	Arg	
205						210			215				220			
tgc	tat	ctg	ctc	gtc	cat	cag	gcc	aaa	agg	ttg	agc	agt	ccc	tgc	atc	783
Cys	Tyr	Leu	Leu	Val	His	Gln	Ala	Lys	Arg	Leu	Ser	Ser	Pro	Cys	Ile	
225						230			235							
atg	gtg	gta	aac	cat	gac	gca	tcc	agc	ata	cct	aga	ctt	aca	gta	gat	831
Met	Val	Val	Asn	His	Asp	Ala	Ser	Ser	Ile	Pro	Arg	Leu	Thr	Val	Asp	
240						245			250							
gtg	gac	gga	agg	aaa	gag	att	ctc	ttc	tat	gat	cga	att	tta	tgt	gat	879
Val	Asp	Gly	Arg	Lys	Glu	Ile	Leu	Phe	Tyr	Asp	Arg	Ile	Leu	Cys	Asp	
255						260			265							
gtc	cct	tgc	agt	ggc	gat	ggc	aca	atg	aga	aaa	aac	att	gat	gtc	tgg	927
Val	Pro	Cys	Ser	Gly	Asp	Gly	Thr	Met	Arg	Lys	Asn	Ile	Asp	Val	Trp	
270						275			280							
aag	aaa	tgg	aca	acc	tta	aac	agc	ttg	cag	ctc	cat	ggc	ctg	cag	ctt	975
Lys	Lys	Trp	Thr	Leu	Asn	Ser	Leu	Gln	Leu	His	Gly	Leu	Gln	Leu		
285						290			295				300			
cgg	att	gca	act	cga	ggt	gct	gag	cag	ctg	gcg	gaa	ggt	ggc	agg	atg	1023
Arg	Ile	Ala	Thr	Arg	Gly	Ala	Glu	Gln	Leu	Ala	Glu	Gly	Gly	Arg	Met	
305						310			315							
gtg	tat	tcc	acg	tgt	tcc	ttg	aac	ccc	gtg	gag	gat	gaa	gca	gtg	atc	1071
Val	Tyr	Ser	Thr	Cys	Ser	Leu	Asn	Pro	Val	Glu	Asp	Glu	Ala	Val	Ile	
320						325			330							
gca	gct	ctg	cta	gag	aag	agt	gaa	gga	gct	ttt	gag	ctt	gct	gat	gtg	1119

Ala Ala Leu Leu Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val			
335	340	345	
tct gct gag ttg cca gga ctg aag tgg atg cct gga gtc tca cag tgg			1167
Ser Ala Glu Leu Pro Gly Leu Lys Trp Met Pro Gly Val Ser Gln Trp			
350	355	360	
aag gtc atg act aga gac ggg cag tgg ttt gca gac tgg cat gag gtt			1215
Lys Val Met Thr Arg Asp Gly Gln Trp Phe Ala Asp Trp His Glu Val			
365	370	375	380
ccc cag ggc agg cat aca caa atc cga cct acc atg ttc cca cca acg			1263
Pro Gln Gly Arg His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Thr			
385	390	395	
gac ctg gag aag cta cag gca atg cat cta gag cga tgc ctt cga atc			1311
Asp Leu Glu Lys Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile			
400	405	410	
ctg ccc cat cat cag aat act gga ggg ttc ttt gtg gca gta ttg gtc			1359
Leu Pro His His Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val			
415	420	425	
aag aaa gca cca atg ccg tgg aac aaa cgt cag ccc aag gtc cag aat			1407
Lys Lys Ala Pro Met Pro Trp Asn Lys Arg Gln Pro Lys Val Gln Asn			
430	435	440	
aaa tct gca gaa gcc aga gaa ccc agg gta tcc agc cat gtg gct gcc			1455
Lys Ser Ala Glu Ala Arg Glu Pro Arg Val Ser Ser His Val Ala Ala			
445	450	455	460
aca gag gga aat ccc agt gac cag tct gag ctg gaa agt cag atg ata			1503
Thr Glu Gly Asn Pro Ser Asp Gln Ser Glu Leu Glu Ser Gln Met Ile			
465	470	475	
act gga gct ggt gac tta gaa aca gct cac aac act gag aat aca gag			1551
Thr Gly Ala Gly Asp Leu Glu Thr Ala His Asn Thr Glu Asn Thr Glu			
480	485	490	
agc aat gag aag aaa gat ggc gtg tgt ggc cct cct cca tca aag aaa			1599
Ser Asn Glu Lys Lys Asp Gly Val Cys Gly Pro Pro Ser Lys Lys			
495	500	505	
atg aag ttg ttt gga ttt aaa gaa gat cca ttt gta ttc att cct gaa			1647
Met Lys Leu Phe Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro Glu			
510	515	520	
gat gat cct tta ttt cca cct att gag aag ttt tat gcc ttg gat cct			1695
Asp Asp Pro Leu Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp Pro			
525	530	535	540
tca ttc ccg agg atg aat ctg tta acc cga acc aca gaa gga aag aag			1743
Ser Phe Pro Arg Met Asn Leu Leu Thr Arg Thr Glu Gly Lys Lys			
545	550	555	
cgg cag ctt tat atg gtc tcc aag gag ctg agg aat gta ctg ctg aac			1791
Arg Gln Leu Tyr Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu Asn			
560	565	570	
aac agc gag aag atg aag gtc att aac act ggg ata aaa gtc tgg tgt			1839

Asn Ser Glu Lys Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp Cys			
575	580	585	
cga aat aac agt ggt gaa gaa ttc gat tgt gca ttc cgt ttg gca cag			1887
Arg Asn Asn Ser Gly Glu Phe Asp Cys Ala Phe Arg Leu Ala Gln			
590	595	600	
gag gga ata tat aca ttg tat cca ttt atc aat tca aga atc atc act			1935
Glu Gly Ile Tyr Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile Thr			
605	610	615	620
gta tca atg gaa gac gtg aag aca ctg ttg acc cag gag aac cca ttc			1983
Val Ser Met Glu Asp Val Lys Thr Leu Thr Gln Glu Asn Pro Phe			
625	630	635	
ttt aga aaa ctg agc agt gag gcc tac agt caa gtc aag gac ctc gca			2031
Phe Arg Lys Leu Ser Ser Glu Ala Tyr Ser Gln Val Lys Asp Leu Ala			
640	645	650	
aag gga agt gtt gtg ctg aag tat gag cca gat tct gcg aat cca gac			2079
Lys Gly Ser Val Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro Asp			
655	660	665	
acc ctc cag tgc ccc atc gtg ctg tgt ggg tgg cgg gga aag gcc tct			2127
Thr Leu Gln Cys Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala Ser			
670	675	680	
att cga act ttt gtg ccc aaa aat gag cgg ctt cat tat ctc agg atg			2175
Ile Arg Thr Phe Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg Met			
685	690	695	700
atg ggt ctg gag gta ctg gga gaa aag aag aaa gag gga gtc att ctt			2223
Met Gly Leu Glu Val Leu Gly Glu Lys Lys Lys Glu Gly Val Ile Leu			
705	710	715	
acc aat gag aat gct gcc agc cca gag cag cct gga gat gag gat gcc			2271
Thr Asn Glu Asn Ala Ala Ser Pro Glu Gln Pro Gly Asp Glu Asp Ala			
720	725	730	
aag cag aca gca caa gac ccc tgc gtc cca gac tcc gtc cct ggc tgt			2319
Lys Gln Thr Ala Gln Asp Pro Cys Val Pro Asp Ser Val Pro Gly Cys			
735	740	745	
gat gca gct gca gct gag cca tcc cgg tga aggagtcttc acacaatgaa			2369
Asp Ala Ala Ala Glu Pro Ser Arg			
750	755		
tttgttaccat ccgttgttgg agatcaaacc tagaatgtcc ttagccaggg acctggaaat			2429
gagtggtggc cacagtctgt taggagtcgc tttgcagag tggatacatg tttctgctgt			2489
taaaggctaa cagccttgc agaagttcag atcccttgtt ggccagtatt gacctagtct			2549
tctaaaacga cagtaaaagt ctacaagtct ttggaaagca gctctatcta tctatgctt			2609
aataactttct ggactgcaca ccagtgtgct gtgcagtcat gctgacactg aggtctcagg			2669
tgacttctgt gcctttgtga taaagggtga gataagccat ctcagaggga aggctggta			2729
atcatgacag cagtttggg gacccttgt gcttatcctg gagttgttt aagtggggtg			2789

gagattgctt gggcatgaa ataaagagct attatgatca tgaaaaaaaaaaaaaaa 2849
aa 2851

<210> 10
<211> 757
<212> PRT
<213> Mouse

<400> 10

Met Gly Arg Arg Ala Arg Gly Arg Arg Phe Gln Gln Pro Pro Gln Pro
1 5 10 15

Glu Gly Glu Glu Asp Ala Ser Asp Gly Gly Arg Lys Arg Gly Gln Ala
20 25 30

Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu Asn Lys Leu Phe
35 40 45

Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu Gly Glu Trp Asp
50 55 60

Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala Thr Leu Arg Ile
65 70 75 80

Thr Gly Tyr Lys Ser His Ala Lys Glu Ile Leu His Cys Leu Lys Asn
85 90 95

Lys Tyr Phe Lys Glu Leu Glu Asp Leu Glu Val Asp Gly Gln Lys Val
100 105 110

Glu Val Pro Gln Pro Leu Ser Trp Tyr Pro Glu Glu Leu Ala Trp His
115 120 125

Thr Asn Leu Ser Arg Lys Ile Leu Arg Lys Ser Pro Leu Leu Ala Lys
130 135 140

Phe His Gln Phe Leu Val Ser Glu Thr Glu Ser Gly Asn Ile Ser Arg
145 150 155 160

Gln Glu Ala Val Ser Met Ile Pro Pro Leu Leu Leu Asn Val Glu Pro
165 170 175

His His Lys Ile Leu Asp Met Cys Ala Ala Pro Gly Ser Lys Thr Thr
180 185 190

Gln Leu Ile Glu Met Leu His Ala Asp Met Ser Val Pro Phe Pro Glu
195 200 205

Gly Phe Val Ile Ala Asn Asp Val Asp Asn Lys Arg Cys Tyr Leu Leu
210 215 220

Val His Gln Ala Lys Arg Leu Ser Ser Pro Cys Ile Met Val Val Asn
225 230 235 240

His Asp Ala Ser Ser Ile Pro Arg Leu Thr Val Asp Val Asp Gly Arg
245 250 255

Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp Val Pro Cys Ser
260 265 270

Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp Lys Lys Trp Thr
275 280 285

Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu Arg Ile Ala Thr
290 295 300

Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Met Val Tyr Ser Thr
305 310 315 320

Cys Ser Leu Asn Pro Val Glu Asp Glu Ala Val Ile Ala Ala Leu Leu
325 330 335

Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val Ser Ala Glu Leu
340 345 350

Pro Gly Leu Lys Trp Met Pro Gly Val Ser Gln Trp Lys Val Met Thr
355 360 365

Arg Asp Gly Gln Trp Phe Ala Asp Trp His Glu Val Pro Gln Gly Arg
370 375 380

His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Thr Asp Leu Glu Lys
385 390 395 400

Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile Leu Pro His His
405 410 415

Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val Lys Lys Ala Pro
420 425 430

Met Pro Trp Asn Lys Arg Gln Pro Lys Val Gln Asn Lys Ser Ala Glu
435 440 445

Ala Arg Glu Pro Arg Val Ser Ser His Val Ala Ala Thr Glu Gly Asn
450 455 460

Pro Ser Asp Gln Ser Glu Leu Glu Ser Gln Met Ile Thr Gly Ala Gly
465 470 475 480

Asp Leu Glu Thr Ala His Asn Thr Glu Asn Thr Glu Ser Asn Glu Lys
485 490 495

Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys Lys Met Lys Leu Phe
500 505 510

Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu
515 520 525

Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg
530 535 540

Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr
545 550 555 560

Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys
565 570 575

Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser
580 585 590

Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr
595 600 605

Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu
610 615 620

Asp Val Lys Thr Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu
625 630 635 640

Ser Ser Glu Ala Tyr Ser Gln Val Lys Asp Leu Ala Lys Gly Ser Val
645 650 655

Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro Asp Thr Leu Gln Cys
660 665 670

Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe
675 680 685

Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu
690 695 700

Val Leu Gly Glu Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Asn
705 710 715 720

Ala Ala Ser Pro Glu Gln Pro Gly Asp Glu Asp Ala Lys Gln Thr Ala
725 730 735

Gln Asp Pro Cys Val Pro Asp Ser Val Pro Gly Cys Asp Ala Ala Ala
740 745 750

Ala Glu Pro Ser Arg
755

<210> 11
<211> 1695
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (14)..(1234)

<400> 11
acttaaggct gcc atg ggg ccc agt gct cct ctg ctg ctc ctc ttc ttt 49
Met Gly Pro Ser Ala Pro Leu Leu Leu Leu Phe Phe
1 5 10

ttg tca tgg acg gga ccc ctt cag gga cag cag cac cac ctt gtg gag 97
Leu Ser Trp Thr Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
15 20 25

tac atg gaa cgc cga cta gct gcc tta gag gaa cgg ctg gcc caa tgc 145
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys
30 35 40

cag gat cag agt agt cgg cat gct gcc gag ctt cgg gac ttc aaa aac 193
Gln Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
45 50 55 60

aag atg ttg cct ctc ctg gag gtg gca gag aag gag cgg gag acc ctc 241
Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu
65 70 75

aga act gaa gca gac tcc atc tca gga aga gtg gac cgt ctt gaa agg 289
Arg Thr Glu Ala Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg
80 85 90

gag gta gac tat ctg gag aca cag aac cca gct ttg ccc tgt gta gag Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu 95 100 105	337
ctg gat gag aag gtg act gga ggt cct gga gcc aaa ggc aag ggc cga Leu Asp Glu Lys Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg 110 115 120	385
aga aat gag aaa tac gat atg gtg acg gac tgt agc tac aca gtc gct Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala 125 130 135 140	433
cag gtg agg tca atg aag atc ctg aag cgg ttt ggt ggt tca gct ggc Gln Val Arg Ser Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly 145 150 155	481
cta tgg acc aag gat ccg ctg ggg cca gca gag aag atc tac gtg tta Leu Trp Thr Lys Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu 160 165 170	529
gac ggc acc cag aac gac acg gct ttt gtc ttc cca agg ctg cgt gac Asp Gly Thr Gln Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp 175 180 185	577
ttc acc ctt gcc atg gct gcc cgg aaa gct tcc cga att cgg gtg ccc Phe Thr Leu Ala Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro 190 195 200	625
ttc ccc tgg gta ggc acg ggg cag ctg gtg tac ggt ggc ttc ctt tat Phe Pro Trp Val Gly Thr Gly Gln Leu Val Tyr Gly Phe Leu Tyr 205 210 215 220	673
tat gct cga agg cct cct gga gga cct gga ggg ggt ggt gaa ttg gag Tyr Ala Arg Arg Pro Pro Gly Gly Pro Gly Gly Gly Glu Leu Glu 225 230 235	721
aac act ctg cag ctg atc aaa ttt cac ttg gca aac cga aca gtg gtg Asn Thr Leu Gln Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val 240 245 250	769
gat agc tca gtg ttc cct gca gag agc ctg ata ccc ccc tac ggc ctg Asp Ser Ser Val Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu 255 260 265	817
aca gca gat aca tat atc gac ctg gca gct gat gag gag ggc ctg tgg Thr Ala Asp Thr Tyr Ile Asp Leu Ala Asp Glu Glu Gly Leu Trp 270 275 280	865
gct gtc tat gcc act cga gat gat gac agg cat ttg tgt cta gcc aag Ala Val Tyr Ala Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys 285 290 295 300	913
tta gac cca cag aca ctt gac aca gag cag cag tgg gac aca cca tgt Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys 305 310 315	961
ccc aga gag aac gca gag gct gtc atc tgt ggg acc ctg tac Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr 320 325 330	1009

gtt gtc tat aac acc cgc cct gcc agt agg gct cgt att cag tgt tcc		1057	
Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser			
335	340	345	
ttc gat gcc agt ggt act ctc gcc cct gaa agg gca gca ctc tcc tat		1105	
Phe Asp Ala Ser Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr			
350	355	360	
ttt cca cgc cga tat ggt gcc cat gcc agc ctt cgc tat aac ccc cgt		1153	
Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg			
365	370	375	380
gag cgc cag ctg tat gcc tgg gat gat ggc tat cag att gtc tac aaa		1201	
Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys			
385	390	395	
ttg gag atg aag aag gag gag gaa gtt taa gcagctagcc ttgtgcttt		1254	
Leu Glu Met Lys Lys Glu Glu Val			
400	405		
gattcttatg cccagacatt tatattcctg ttagctctcc tgcagttcat ccttcaaaac		1314	
gaaggccagt ggtggtagct catataccct aatttctaaa ggacaaccaa attctcaagc		1374	
ccctctgttt tatgcagaac tccagatcct gggtagcatt ttagaactga acagcaaaca		1434	
aacaccctaa atcttcactc ctgccctatg tccacaaaagt ttagttccaa actcagagcc		1494	
ctgtcctttg gagagggtca accccagaca gcaggcgaca gcattctgc cctcagtagt		1554	
accgaaggga gagaactcag agacaaagct gccctccctc cttccccct ccagtgttagg		1614	
ggagaatggg gctttccccca catcacttg tatggtaaca gtttgcatta aaaggaaaac		1674	
ccacaaaaaaaaaaaaaaaaa a		1695	

<210> 12
 <211> 406
 <212> PRT
 <213> Mouse

 <400> 12

Met Gly Pro Ser Ala Pro Leu Leu Leu Phe Phe Leu Ser Trp Thr
 1 5 10 15

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 20 25 30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
 35 40 45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
 50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu Arg Thr Glu Ala
65 70 75 80

Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Leu Asp Glu Lys
100 105 110

Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg Arg Asn Glu Lys
115 120 125

Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala Gln Val Arg Ser
130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly Leu Trp Thr Lys
145 150 155 160

Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro Phe Pro Trp Val
195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Tyr Ala Arg Arg
210 215 220

Pro Pro Gly Gly Pro Gly Gly Glu Leu Glu Asn Thr Leu Gln
225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
245 250 255

Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
275 280 285

Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
340 345 350

Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr Phe Pro Arg Arg
355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Lys
385 390 395 400

Lys Lys Glu Glu Val
405

<210> 13
<211> 1610
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (48)..(1193)

<400> 13
gctgggtact aggagaagcc atcatgcaca cctctactga agccagg atg ggc atg 56
Met Gly Met
1

agg gcg gca ctg aca ggc ttt gcg gtc ctg atg ctg ctc cag agc tgc 104
Arg Ala Ala Leu Thr Gly Phe Ala Val Leu Met Leu Leu Gln Ser Cys
5 10 15

tct gcg tac aag ctg gtc tgc tac ttc acc agc tgg tcc cag tac cgg 152
Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser Gln Tyr Arg
20 25 30 35

gaa ggc gtt gga agc ttc tta cca gac gcc atc caa cct ttc ctg tgc 200
Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro Phe Leu Cys
40 45 50

acc cac atc atc tac agc ttt gcc aac atc agc agc gac aac atg ctt 248
Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp Asn Met Leu
55 60 65

agc aca tgg gag tgg aat gac gag tcg aac tat gac aag ctg aat aaa 296

Ser	Thr	Trp	Glu	Trp	Asn	Asp	Glu	Ser	Asn	Tyr	Asp	Lys	Leu	Asn	Lys	
70					75						80					
ctg	aag	acc	aga	aac	acc	aac	ctg	aag	acc	ctc	ctg	tct	gtt	gga	ggg	344
Leu	Lys	Thr	Arg	Asn	Thr	Asn	Leu	Lys	Thr	Leu	Leu	Ser	Val	Gly	Gly	
85					90						95					
tgg	aaa	ttt	ggc	gaa	aaa	aga	ttt	tcc	gag	att	gcc	tcc	aac	act	gag	392
Trp	Lys	Phe	Gly	Glu	Lys	Arg	Phe	Ser	Glu	Ile	Ala	Ser	Asn	Thr	Glu	
100					105					110				115		
aga	cgc	act	gct	ttc	gtc	cg	tcg	gta	gcc	ccg	tcc	ctg	cgt	tct	tat	440
Arg	Arg	Thr	Ala	Phe	Val	Arg	Ser	Val	Ala	Pro	Phe	Leu	Arg	Ser	Tyr	
120					125					130						
ggc	ttt	gat	ggg	ctg	gat	ctc	gcc	tgg	ctc	tac	cct	cg	tta	aga	gac	488
Gly	Phe	Asp	Gly	Leu	Asp	Leu	Ala	Trp	Leu	Tyr	Pro	Arg	Leu	Arg	Asp	
135					140					145						
aag	cag	tat	ttc	tcc	acc	ctg	atc	aag	gaa	ctg	aat	g	gaa	ttc	aca	536
Lys	Gln	Tyr	Phe	Ser	Thr	Leu	Ile	Lys	Glu	Leu	Asn	Ala	Glu	Phe	Thr	
150					155					160						
aag	gag	gtc	cag	cca	ggc	aga	gag	aaa	ctc	ctg	ctc	agc	gca	gct	ttg	584
Lys	Glu	Val	Gln	Pro	Gly	Arg	Glu	Lys	Leu	Leu	Leu	Ser	Ala	Ala	Leu	
165					170					175						
tca	gca	gga	aag	gtg	gcc	att	gac	act	ggc	tat	gac	atc	gcc	cag	ata	632
Ser	Ala	Gly	Lys	Val	Ala	Ile	Asp	Thr	Gly	Tyr	Asp	Ile	Ala	Gln	Ile	
180					185					190			195			
gcc	caa	cac	ctg	gat	ttt	atc	aat	ctc	atg	acc	tac	gat	ttc	cat	gga	680
Ala	Gln	His	Leu	Asp	Phe	Ile	Asn	Leu	Met	Thr	Tyr	Asp	Phe	His	Gly	
200					205					210						
gtc	tgg	cgc	caa	atc	aca	ggc	cat	cac	agc	ccc	ctc	ttc	caa	ggc	cag	728
Val	Trp	Arg	Gln	Ile	Thr	Gly	His	His	Ser	Pro	Leu	Phe	Gln	Gly	Gln	
215					220					225						
aag	gac	act	agg	ttt	gac	aga	tac	agc	aat	gtg	aac	tat	gcc	gtg	cag	776
Lys	Asp	Thr	Arg	Phe	Asp	Arg	Tyr	Ser	Asn	Val	Asn	Tyr	Ala	Val	Gln	
230					235					240						
tac	atg	ata	cgt	ctg	gga	gcc	cag	gcc	agc	aag	cta	ctg	atg	ggc	atc	824
Tyr	Met	Ile	Arg	Leu	Gly	Ala	Gln	Ala	Ser	Lys	Leu	Leu	Met	Gly	Ile	
245					250					255						
ccc	acc	ttt	ggg	aag	agc	ttc	act	ctg	gca	tct	tct	gaa	aat	cag	ttg	872
Pro	Thr	Phe	Gly	Lys	Ser	Phe	Thr	Leu	Ala	Ser	Ser	Glu	Asn	Gln	Leu	
260					265					270			275			
gga	gct	cca	atc	tca	ggg	gaa	tta	cca	ggc	cg	ttc	acc	aag	gag	920	
Gly	Ala	Pro	Ile	Ser	Gly	Glu	Gly	Leu	Pro	Gly	Arg	Phe	Thr	Lys	Glu	
280					285					290						
gca	ggg	acc	ctg	gcc	tac	tac	gag	ata	tgc	gac	ttc	ctc	aaa	gga	gct	968
Ala	Gly	Thr	Leu	Ala	Tyr	Tyr	Glu	Ile	Cys	Asp	Phe	Leu	Lys	Gly	Ala	
295					300					305						
gaa	gta	cat	cga	ctc	tcc	aac	gag	aag	gtt	ccc	ttc	gct	acc	aag	ggc	1016

Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala Thr Lys Gly			
310	315	320	
aac cag tgg gtg ggg tat gag gac aag gag agt gtc aaa aac aag gtt			1064
Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys Asn Lys Val			
325	330	335	
ggg ttc ctg aag gag aag aag ctg gca gga gcc atg gtg tgg gca ctg			1112
Gly Phe Leu Lys Glu Lys Leu Ala Gly Ala Met Val Trp Ala Leu			
340	345	350	355
gat ttg gat gat ttc cag ggc acc tgt cag ccg aag gaa ttc ttc ccg			1160
Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu Phe Phe Pro			
360	365	370	
ctc acc aac gcc atc aag gat gcc ctg gct tag ctccccctt cccatatggt			1213
Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala			
375	380		
accccccactc tctggccagg agtttaatct cttgcaatgt taagtccccc aactgagcct			1273
cagtttctcc ttcccttggc acctgtgtaa ggggccacag caggctcagc tatggagaac			1333
agggaactag ggttaggacga tgggtggggtt gtgagagtca cagtgtgagc agatacacaa			1393
ccctgttaag gaatgcaaat tctcagactc taacctccct ttacccagcc tgaccaaagg			1453
acaccacttgc atcaagtag gcaaataatct tacaggattt agggaccata ctaattatac			1513
cctctgcaaa gcccaacttgc aatcccttccc ttaggaactt aatcgtccca cttcccttgc			1573
cctaatttcca cagctgttca ataaagcgcc agaacct			1610
<210> 14			
<211> 381			
<212> PRT			
<213> Mouse			
<400> 14			
Met Gly Met Arg Ala Ala Leu Thr Gly Phe Ala Val Leu Met Leu Leu			
1	5	10	15
Gln Ser Cys Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser			
20	25	30	
Gln Tyr Arg Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro			
35	40	45	
Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp			
50	55	60	
Asn Met Leu Ser Thr Trp Glu Trp Asn Asp Glu Ser Asn Tyr Asp Lys			
65	70	75	80

Leu Asn Lys Leu Lys Thr Arg Asn Thr Asn Leu Lys Thr Leu Leu Ser
85 90 95

Val Gly Gly Trp Lys Phe Gly Glu Lys Arg Phe Ser Glu Ile Ala Ser
100 105 110

Asn Thr Glu Arg Arg Thr Ala Phe Val Arg Ser Val Ala Pro Phe Leu
115 120 125

Arg Ser Tyr Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Arg
130 135 140

Leu Arg Asp Lys Gln Tyr Phe Ser Thr Leu Ile Lys Glu Leu Asn Ala
145 150 155 160

Glu Phe Thr Lys Glu Val Gln Pro Gly Arg Glu Lys Leu Leu Leu Ser
165 170 175

Ala Ala Leu Ser Ala Gly Lys Val Ala Ile Asp Thr Gly Tyr Asp Ile
180 185 190

Ala Gln Ile Ala Gln His Leu Asp Phe Ile Asn Leu Met Thr Tyr Asp
195 200 205

Phe His Gly Val Trp Arg Gln Ile Thr Gly His His Ser Pro Leu Phe
210 215 220

Gln Gly Gln Lys Asp Thr Arg Phe Asp Arg Tyr Ser Asn Val Asn Tyr
225 230 235 240

Ala Val Gln Tyr Met Ile Arg Leu Gly Ala Gln Ala Ser Lys Leu Leu
245 250 255

Met Gly Ile Pro Thr Phe Gly Lys Ser Phe Thr Leu Ala Ser Ser Glu
260 265 270

Asn Gln Leu Gly Ala Pro Ile Ser Gly Glu Gly Leu Pro Gly Arg Phe
275 280 285

Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu
290 295 300

Lys Gly Ala Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala
305 310 315 320

Thr Lys Gly Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys
325 330 335

Asn Lys Val Gly Phe Leu Lys Glu Lys Lys Leu Ala Gly Ala Met Val
340 345 350

Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu
355 360 365

Phe Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala
370 375 380

<210> 15
<211> 2002
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (178)..(1689)

<400> 15
gaattccgga agggggctct gaccgttcc gagcgccaaac gcagcctctg tagcccgcaa 60
gtcttcgtcg cttgctccgg gctctgaagt ccggggccac caggggcccgc agcgctgggg 120
ggtcggtcta gctgcgagga tccgggctgc ccacgaagcg aagggcgggc gcccagg 177
atg gga tgc gtg aag tcc agg ttc ctc cga gat gga agc aag gcc tca 225
Met Gly Cys Val Lys Ser Arg Phe Leu Arg Asp Gly Ser Lys Ala Ser
1 5 10 15
aaa aca gag cca agt gcc aat cag aag ggc cct gtg tat gtg ccg gat 273
Lys Thr Glu Pro Ser Ala Asn Gln Lys Gly Pro Val Tyr Val Pro Asp
20 25 30
ccc acg tcc tcc agc aag ctg gga cca aac aac agc aac agc atg ccc 321
Pro Thr Ser Ser Lys Leu Gly Pro Asn Asn Ser Asn Ser Met Pro
35 40 45
cca ggg ttt gtg gag ggc tct gag gat acc att gtg gtc gca ctg tac 369
Pro Gly Phe Val Glu Gly Ser Glu Asp Thr Ile Val Val Ala Leu Tyr
50 55 60
gac tat gag gct att cac cgt gaa gac ctc agc ttc cag aag gga gac 417
Asp Tyr Glu Ala Ile His Arg Glu Asp Leu Ser Phe Gln Lys Gly Asp
65 70 75 80
cag atg gtg gtt ctg gag gag gct ggg gag tgg tgg aag gca cgg tcc 465
Gln Met Val Val Leu Glu Ala Gly Glu Trp Trp Lys Ala Arg Ser
85 90 95
ctg gct acc aag aag gaa ggc tac atc cca agc aac tat gtg gct cga 513
Leu Ala Thr Lys Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg

100	105	110	
gtt aac tct ttg gag aca gaa gag tgg ttc ttc aag ggg atc agc cgg Val Asn Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg 115	120	125	561
aag gat gca gag cgc cac ctc ctg gct cca ggc aac atg ctg ggc tcc Lys Asp Ala Glu Arg His Leu Leu Ala Pro Gly Asn Met Leu Gly Ser 130	135	140	609
ttc atg atc cgg gac agt gag acc acc aaa ggg agc tac tcg ttg tct Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser 145	150	155	657
gtt cga gac ttt gac ccc cag cac gga gac acc gtg aag cac tat aag Val Arg Asp Phe Asp Pro Gln His Gly Asp Thr Val Lys His Tyr Lys 165	170	175	705
atc cgg acg ctg gac agt gga ggc ttc tac atc tct cca agg agc acc Ile Arg Thr Leu Asp Ser Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr 180	185	190	753
ttc agc agc ctg cag gaa ctc gtg ctc cac tac aag aag ggg aag gat Phe Ser Ser Leu Gln Glu Leu Val Leu His Tyr Lys Lys Gly Lys Asp 195	200	205	801
ggg ctc tgc cag aag ctg tca gtg ccc tgt gtg tct ccc aaa ccc cag Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Val Ser Pro Lys Pro Gln 210	215	220	849
aag cca tgg gag aaa gat gct tgg gag att cct cga gaa tcc ctc cag Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Gln 225	230	235	897
atg gag aag aaa ctt gga gct ggg cag ttt gga gaa gtg tgg atg gcc Met Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala 245	250	255	945
acc tac aac aag cac acc aaa gtg gcg gtg aag aca atg aag cca ggg Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly 260	265	270	993
agc atg tcc gtg gag gcc ttc ctg gct gag gcc aac ctg atg aag tcg Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser 275	280	285	1041
ctg cag cat gac aaa ctg gtg aag cta cac gct gtg gtc tct cag gag Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu 290	295	300	1089
ccc atc ttt att gtc acg gag ttc atg gcc aaa gga agc ctg ctg gac Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp 305	310	315	1137
ttt ctc aag agt gaa gaa ggc agc aag cag cca ctg cca aaa ctc att Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile 325	330	335	1185
gac ttc tca gcc cag atc tca gaa ggc atg gcc ttc att gag cag agg Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg			1233

340	345	350	
aac tac atc cac cga gac ctg agg gct gcc aac atc tta gtc tct gca Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala 355	360	365	1281
tca ctg gtg tgt aag att gct gac ttt gga ctg gca cga atc atc gag Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu 370	375	380	1329
gac aat gag tac aca gct cgg gaa gga gcc aag ttc ccc atc aag tgg Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp 385	390	395	1377
aca gct cct gaa gcc atc aac ttt ggt tcc ttc acc atc aag tca gat Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp 405	410	415	1425
gtc tgg tcc ttt ggt atc ctg ctg atg gaa att gtc acc tat ggc cgg Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg 420	425	430	1473
atc cct tac cca ggt atg tca aac cca gag gtg att cgg gca cta gag Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu 435	440	445	1521
cat ggg tac cgt atg cct cga cca gat aac tgt cca gaa gag ctc tac His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr 450	455	460	1569
aat atc atg atc cgc tgc tgg aag aac cgc ccc gag gaa cgg ccc acc Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr 465	470	475	1617
ttt gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc act gag Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu 485	490	495	1665
agc cag tat cag cag cag cct tga cagcagtaag gacatgagca gagccagaag Ser Gln Tyr Gln Gln Pro 500			1719
ccccatcagt gccttgacac gccccacttg ctggggccac tctcagacac cacaccacac acactgcagc tggtgagtgg gtgggaggac ttccacaatct ctttctgact ctagtcatct gcaatccgcc actctcaggg cctccaagtt ggtatgtctc atttgcctgg aatgactgaa ttcaatctat agctgtgatt taagtggaaa ctgttagaat agtatttaaa taaaagatat gaatgtcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa			1779 1839 1899 1959 2002

<210> 16
 <211> 503
 <212> PRT
 <213> Mouse

<400> 16

Met Gly Cys Val Lys Ser Arg Phe Leu Arg Asp Gly Ser Lys Ala Ser
1 5 10 15

Lys Thr Glu Pro Ser Ala Asn Gln Lys Gly Pro Val Tyr Val Pro Asp
20 25 30

Pro Thr Ser Ser Ser Lys Leu Gly Pro Asn Asn Ser Asn Ser Met Pro
35 40 45

Pro Gly Phe Val Glu Gly Ser Glu Asp Thr Ile Val Val Ala Leu Tyr
50 55 60

Asp Tyr Glu Ala Ile His Arg Glu Asp Leu Ser Phe Gln Lys Gly Asp
65 70 75 80

Gln Met Val Val Leu Glu Glu Ala Gly Glu Trp Trp Lys Ala Arg Ser
85 90 95

Leu Ala Thr Lys Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg
100 105 110

Val Asn Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg
115 120 125

Lys Asp Ala Glu Arg His Leu Leu Ala Pro Gly Asn Met Leu Gly Ser
130 135 140

Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser
145 150 155 160

Val Arg Asp Phe Asp Pro Gln His Gly Asp Thr Val Lys His Tyr Lys
165 170 175

Ile Arg Thr Leu Asp Ser Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr
180 185 190

Phe Ser Ser Leu Gln Glu Leu Val Leu His Tyr Lys Lys Gly Lys Asp
195 200 205

Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Val Ser Pro Lys Pro Gln
210 215 220

Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Gln
225 230 235 240

Met Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala
245 250 255

Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly
260 265 270

Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser
275 280 285

Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu
290 295 300

Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp
305 310 315 320

Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile
325 330 335

Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg
340 345 350

Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala
355 360 365

Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu
370 375 380

Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp
385 390 395 400

Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp
405 410 415

Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg
420 425 430

Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu
435 440 445

His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr
450 455 460

Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr
465 470 475 480

Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu
485 490 495

Ser Gln Tyr Gln Gln Gln Pro
500

<210> 17
<211> 3064
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (133) .. (2463)

<400> 17
ctcactttgc ccgggtcccg ggaggccgtc gacttatcct aggagctcg agctttctt 60
ctgggcaacc agggcgcttc cagacagagt tcctgctgcc acccaccacc cccctctcag 120
cacaggacaa gg atg gag ctc cat ttt ggc tcc tgc ctc tcc ggc tgt ttg 171
Met Glu Leu His Phe Gly Ser Cys Leu Ser Gly Cys Leu
1 5 10
gct ctg ctt gtc ttg ctg cct tcc ctg agc cta gca cag tac gag ggc 219
Ala Leu Leu Val Leu Leu Pro Ser Leu Ser Leu Ala Gln Tyr Glu Gly
15 20 25
tgg ccc tac cag ctc cag tac cct gag tac ttc cag cag ccc gct cct 267
Trp Pro Tyr Gln Leu Gln Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro
30 35 40 45
gag cac cat cag cggtt ccc tcc gat gtg gtc aag atc cag gtc 315
Glu His His Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val
50 55 60
cgc ctg gcg ggc cag aag agg aag cac aat gag ggc cgc gtg gag gtc 363
Arg Leu Ala Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val
65 70 75
tac tac gaa ggc cag tgg ggc acg gtg tgc gac gat gac ttc tcg atc 411
Tyr Tyr Glu Gly Gln Trp Gly Thr Val Cys Asp Asp Phe Ser Ile
80 85 90
cat gcc gcc cat gtg gtc tgc cgg caa gtg ggc tat gta gag gcc aag 459
His Ala Ala His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys
95 100 105
tcc tgg gct gcc agc tcc tcc tac ggt cca ggc gaa ggc ccc atc tgg 507
Ser Trp Ala Ala Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp
110 115 120 125
ttg gac aat atc tac tgt act ggc aaa gag tcg acc ctg gca tct tgc 555
Leu Asp Asn Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys
130 135 140
tcc tcc aat ggc tgg ggt gtc act gac tgc aag cac act gaa gac gtt 603

Ser Ser Asn Gly Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val			
145	150	155	
gga gtg gtg tgt agt gag aaa aga att cct ggc ttc aaa ttt gac aat			651
Gly Val Val Cys Ser Glu Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn			
160	165	170	
tcg ttg atc aac caa ata gag agc cta aat ata cag gtg gaa gac atc			699
Ser Leu Ile Asn Gln Ile Glu Ser Leu Asn Ile Gln Val Glu Asp Ile			
175	180	185	
cgg att cgg ccc atc ctt tct gcc ttt cgc cat cgc aag cct gtg aca			747
Arg Ile Arg Pro Ile Leu Ser Ala Phe Arg His Arg Lys Pro Val Thr			
190	195	200	205
gag ggc tac gtg gag gtg aag gag ggc aag gct tgg aag cag atc tgc			795
Glu Gly Tyr Val Glu Val Lys Glu Gly Lys Ala Trp Lys Gln Ile Cys			
210	215	220	
aac aaa cac tgg aca gcc aag aat tcc cac gtg gtc tgt ggc atg ttc			843
Asn Lys His Trp Thr Ala Lys Asn Ser His Val Val Cys Gly Met Phe			
225	230	235	
ggc ttc cct gca gag aag acc tac aac ccc aaa gcc tat aaa acc ttt			891
Gly Phe Pro Ala Glu Lys Thr Tyr Asn Pro Lys Ala Tyr Lys Thr Phe			
240	245	250	
gcc tcg cgg agg aag ctg cgt tac tgg aag ttt tct atg aac tgc acg			939
Ala Ser Arg Arg Lys Leu Arg Tyr Trp Lys Phe Ser Met Asn Cys Thr			
255	260	265	
ggc act gaa gcg cat atc tcc agc tgc aag ctg ggc cct tcc gtg acc			987
Gly Thr Glu Ala His Ile Ser Ser Cys Lys Leu Gly Pro Ser Val Thr			
270	275	280	285
cgg gac cct gtg aag aac gcc acc tgt gag aac ggg cag cca gct gtg			1035
Arg Asp Pro Val Lys Asn Ala Thr Cys Glu Asn Gly Gln Pro Ala Val			
290	295	300	
gtc agt tgt gtg cct agc cag atc ttc agc ccc gat gga ccc tca agg			1083
Val Ser Cys Val Pro Ser Gln Ile Phe Ser Pro Asp Gly Pro Ser Arg			
305	310	315	
ttc cgg aaa gcc tac aag cca gag caa ccc ttg gtg cgc ctg aga ggt			1131
Phe Arg Lys Ala Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly			
320	325	330	
gga gcc cag gtc ggg gag ggc cga gtg gag gtg ctg aag aat gga gaa			1179
Gly Ala Gln Val Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu			
335	340	345	
tgg gga acc atc tgc gat gac aag tgg gac ctg gta tct gcc agt gtg			1227
Trp Gly Thr Ile Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val			
350	355	360	365
gtc tgc cga gag ctg ggc ttt ggg acc gct aaa gag gcc atc aca ggc			1275
Val Cys Arg Glu Leu Gly Phe Gly Thr Ala Lys Glu Ala Ile Thr Gly			
370	375	380	
tcc aga cta ggg caa ggg att ggg ccc atc cat ctc aat gaa gtc cag			1323

Ser Arg Leu Gly Gln Gly Ile Gly Pro Ile His Leu Asn Glu Val Gln			
385	390	395	
tgc aca ggg act gag aag tcc atc ata gac tgc aaa ttc aac aca gag			1371
Cys Thr Gly Thr Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Thr Glu			
400	405	410	
tct caa ggc tgc aac cat gaa gaa gat gcc ggg gtg cga tgc aac atc			1419
Ser Gln Gly Cys Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Ile			
415	420	425	
ccc atc atg ggt ttc cag aaa aag gtg cgc ctg aat gga ggc cgc aat			1467
Pro Ile Met Gly Phe Gln Lys Lys Val Arg Leu Asn Gly Gly Arg Asn			
430	435	440	445
cct tat gag ggc cga gtg gag gtg cta aca gag aga aat ggg tcc ctt			1515
Pro Tyr Glu Gly Arg Val Glu Val Leu Thr Glu Arg Asn Gly Ser Leu			
450	455	460	
gtt tgg ggg act gta tgc ggc cag aac tgg ggc att gtg gaa gcc atg			1563
Val Trp Gly Thr Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met			
465	470	475	
gtg gtc tgc cgg cag cta ggc ctg ggc ttt gcc agc aat gcc ttt cag			1611
Val Val Cys Arg Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln			
480	485	490	
gag acc tgg tac tgg cat gga aat atc ttc gcc aac aac gtg gtc atg			1659
Glu Thr Trp Tyr Trp His Gly Asn Ile Phe Ala Asn Asn Val Val Met			
495	500	505	
agt gga gtg aag tgc tca gga acg gag ctg tcc cta gca cac tgc cgc			1707
Ser Gly Val Lys Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg			
510	515	520	525
cat gac gag gag gtg gcc tgc ccc gag ggc ggg gtg cgg ttt ggt gct			1755
His Asp Glu Glu Val Ala Cys Pro Glu Gly Gly Val Arg Phe Gly Ala			
530	535	540	
gga gtc gcc tgc tcg gaa act gca cct gac ctg gtg ctt aat gct gag			1803
Gly Val Ala Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu			
545	550	555	
att gtc cag cag act gcc tac ctg gag gac agg ccc atg tcc ttg ctg			1851
Ile Val Gln Gln Thr Ala Tyr Leu Glu Asp Arg Pro Met Ser Leu Leu			
560	565	570	
cag tgt gcc atg gag gag aac tgc ctc tcc gcc tcc gct gtg cac acc			1899
Gln Cys Ala Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Val His Thr			
575	580	585	
gac ccc acc aga ggc cac cgg cgc ctt tta cgc ttc tcc tcc cag atc			1947
Asp Pro Thr Arg Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile			
590	595	600	605
cac aac aat ggc cag tct gac ttc cgc ccc aag aat ggc cgc cat gcg			1995
His Asn Asn Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala			
610	615	620	
tgg att tgg cac gac tgc cac agg cac tac cac agc atg gaa gtc ttc			2043

Trp Ile Trp His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe		
625	630	635
act tac tat gac ctg ctg agc ctc aac ggc acc aag gtg gct gag ggc		2091
Thr Tyr Asp Leu Leu Ser Leu Asn Gly Thr Lys Val Ala Glu Gly		
640	645	650
cac aag gcc agc ttc tgc ctg gag gac act gag tgt gag gga gac att		2139
His Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile		
655	660	665
cag aag agt tac gag tgt gcc aac ttt gga gaa caa ggc atc acc atg		2187
Gln Lys Ser Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Met		
670	675	680
685		
ggc tgc tgg gac atg tac cgt cat gac att gac tgc cag tgg ata gac		2235
Gly Cys Trp Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp		
690	695	700
atc acc gat gtg ccc cct gga gac tac ctg ttc cag gtt gtc att aac		2283
Ile Thr Asp Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn		
705	710	715
ccc aac tat gaa gtg cca gaa tca gat ttc tct aac aac atc atg aag		2331
Pro Asn Tyr Glu Val Pro Glu Ser Asp Phe Ser Asn Asn Ile Met Lys		
720	725	730
tgc agg agc cgc tat gat ggc tac cgc atc tgg atg tac aac tgt cac		2379
Cys Arg Ser Arg Tyr Asp Gly Tyr Arg Ile Trp Met Tyr Asn Cys His		
735	740	745
gta ggt gga gcc ttc agt gag gag aca gaa cag aag ttc gaa cac ttc		2427
Val Gly Gly Ala Phe Ser Glu Glu Thr Glu Gln Lys Phe Glu His Phe		
750	755	760
765		
agt gga ctt cta aat aac cag ctc tct gta cag taa agaagatcct		2473
Ser Gly Leu Leu Asn Asn Gln Leu Ser Val Gln		
770	775	
gggccaggca tgatggctca tgcctgtaat ccctgcactc atgctgaggc aggaggatg		2533
ccacaagatt tccactctgg acattaaacc aagcttcagt ttcaaaagaa atgaatgaaa		2593
gaaaggaagg aaggaaggaa ggaaggaagg aaggaaggaa ggaaggaagg aagaaagggg		2653
aaaggaaag ggaagaaaaa tgacttaatg gtcaacttact gactcctggg ggaatactga		2713
ttaccacctc tttcttagcc agatccagct gagaagaaag gtgctcattc actccccaga		2773
cactgccgtg tgcctgtc ctgaggcctt aggggcaggg ctggggcaca tggccatgga		2833
aacttcatgtca caagcttgcgac gcagcttgcgc ccatccgagc tttggcatgt cccaaatgttg		2893
acatcatctg tgctctgcac agagggccg tttcttctg ggaacacagc aggcatgaac		2953
tcagcaactg cagaggtgat cgggctgaac tccgttttc cccttcttag gtcatttctg		3013
gaaaacttga atatcaagac ctctgtatata agtttggttt gttttttgtt t		3064

<210> 18
<211> 776
<212> PRT
<213> Mouse

<400> 18

Met Glu Leu His Phe Gly Ser Cys Leu Ser Gly Cys Leu Ala Leu Leu
1 5 10 15

Val Leu Leu Pro Ser Leu Ser Leu Ala Gln Tyr Glu Gly Trp Pro Tyr
20 25 30

Gln Leu Gln Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu His His
35 40 45

Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val Arg Leu Ala
50 55 60

Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val Tyr Tyr Glu
65 70 75 80

Gly Gln Trp Gly Thr Val Cys Asp Asp Phe Ser Ile His Ala Ala
85 90 95

His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys Ser Trp Ala
100 105 110

Ala Ser Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp Leu Asp Asn
115 120 125

Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys Ser Ser Asn
130 135 140

Gly Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val
145 150 155 160

Cys Ser Glu Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile
165 170 175

Asn Gln Ile Glu Ser Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg
180 185 190

Pro Ile Leu Ser Ala Phe Arg His Arg Lys Pro Val Thr Glu Gly Tyr
195 200 205

Val Glu Val Lys Glu Gly Lys Ala Trp Lys Gln Ile Cys Asn Lys His

210

215

220

Trp Thr Ala Lys Asn Ser His Val Val Cys Gly Met Phe Gly Phe Pro
225 230 235 240

Ala Glu Lys Thr Tyr Asn Pro Lys Ala Tyr Lys Thr Phe Ala Ser Arg
245 250 255

Arg Lys Leu Arg Tyr Trp Lys Phe Ser Met Asn Cys Thr Gly Thr Glu
260 265 270

Ala His Ile Ser Ser Cys Lys Leu Gly Pro Ser Val Thr Arg Asp Pro
275 280 285

Val Lys Asn Ala Thr Cys Glu Asn Gly Gln Pro Ala Val Val Ser Cys
290 295 300

Val Pro Ser Gln Ile Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys
305 310 315 320

Ala Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Ala Gln
325 330 335

Val Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr
340 345 350

Ile Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg
355 360 365

Glu Leu Gly Phe Gly Thr Ala Lys Glu Ala Ile Thr Gly Ser Arg Leu
370 375 380

Gly Gln Gly Ile Gly Pro Ile His Leu Asn Glu Val Gln Cys Thr Gly
385 390 395 400

Thr Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Thr Glu Ser Gln Gly
405 410 415

Cys Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Ile Pro Ile Met
420 425 430

Gly Phe Gln Lys Lys Val Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu
435 440 445

Gly Arg Val Glu Val Leu Thr Glu Arg Asn Gly Ser Leu Val Trp Gly

450

455

460

Thr Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys
465 470 475 480

Arg Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp
485 490 495

Tyr Trp His Gly Asn Ile Phe Ala Asn Asn Val Val Met Ser Gly Val
500 505 510

Lys Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Glu
515 520 525

Glu Val Ala Cys Pro Glu Gly Gly Val Arg Phe Gly Ala Gly Val Ala
530 535 540

Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Ile Val Gln
545 550 555 560

Gln Thr Ala Tyr Leu Glu Asp Arg Pro Met Ser Leu Leu Gln Cys Ala
565 570 575

Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Val His Thr Asp Pro Thr
580 585 590

Arg Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn
595 600 605

Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp
610 615 620

His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr Tyr Tyr
625 630 635 640

Asp Leu Leu Ser Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala
645 650 655

Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Ser
660 665 670

Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Met Gly Cys Trp
675 680 685

Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp

690

695

700

Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Tyr
 705 710 715 720

Glu Val Pro Glu Ser Asp Phe Ser Asn Asn Ile Met Lys Cys Arg Ser
 725 730 735

Arg Tyr Asp Gly Tyr Arg Ile Trp Met Tyr Asn Cys His Val Gly Gly
 740 745 750

Ala Phe Ser Glu Glu Thr Glu Gln Lys Phe Glu His Phe Ser Gly Leu
 755 760 765

Leu Asn Asn Gln Leu Ser Val Gln
 770 775

<210> 19
 <211> 3276
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (148)..(2763)

<400> 19
 ttgggccagt ggcctgtcac tgggttctcc gctcttatgt tggaaagtgt gagggacaca 60
 ggagcgacct gcataacctga gcctccgaga gagaagctgc actctggcat ccagtagcag 120
 caggagacta agcagataaa aggagcc atg act tct ggc gct agt cat atg ctg 174
 Met Thr Ser Gly Ala Ser His Met Leu
 1 5
 gaa gct gcc ctg gag cag atg gac ggg atc att gca ggc act aaa aca 222
 Glu Ala Ala Leu Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr
 10 15 20 25
 gct gca gat ttt agt gat ggt acc tgt gag cct ggg ctg tct ccc cca 270
 Ala Ala Asp Phe Ser Asp Gly Thr Cys Glu Pro Gly Leu Ser Pro Pro
 30 35 40
 tcc acc tgc ttg aac tcc atg cct gtg ctc cat ctc att gag gac ctg 318
 Ser Thr Cys Leu Asn Ser Met Pro Val Leu His Leu Ile Glu Asp Leu
 45 50 55
 aga cta gcc ttg gag atg ttg gca ctt cct cag gaa aga gaa gcc ctc 366
 Arg Leu Ala Leu Glu Met Leu Ala Leu Pro Gln Glu Arg Glu Ala Leu
 60 65 70
 ctg agc cag gtc cct ggc cca aca gct acc tac ata aag gag tgg ttt 414
 Leu Ser Gln Val Pro Gly Pro Thr Ala Thr Tyr Ile Lys Glu Trp Phe

75

80

85

gag gac agc ttg tcc cag gta aat cac cac ggt gct gct agt aat gaa	462
Glu Asp Ser Leu Ser Gln Val Asn His His Gly Ala Ala Ser Asn Glu	
90 95 100 105	
acc tac cag gaa cgc ctg gca cgg cta gaa gga gat aaa gag tcc ctc	510
Thr Tyr Gln Glu Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu	
110 115 120	
ata cta cag gtg agc gtc ctc aca gat caa gtg gaa gcc caa gga gag	558
Ile Leu Gln Val Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu	
125 130 135	
aag att cgg gac ctt gaa gtg tgt ctg gaa ggc cac cag gtg aag ctc	606
Lys Ile Arg Asp Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu	
140 145 150	
aat gct gca gaa gag atg ctt cag cag gag ctg cta agt cgc aca tct	654
Asn Ala Ala Glu Glu Met Leu Gln Gln Glu Leu Leu Ser Arg Thr Ser	
155 160 165	
ctg gag acc cag aag ttg gat ctg atg act gag gtg tct gag ctg aag	702
Leu Glu Thr Gln Lys Leu Asp Leu Met Thr Glu Val Ser Glu Leu Lys	
170 175 180 185	
ctc aag ctg gtt ggt atg gaa aaa gaa cag aaa gaa caa gaa gaa aaa	750
Leu Lys Leu Val Gly Met Glu Lys Glu Gln Lys Glu Gln Glu Glu Lys	
190 195 200	
cag aga aaa gca gag gag tta ctg caa gag ctt aag cac ctc aaa atc	798
Gln Arg Lys Ala Glu Glu Leu Leu Gln Glu Leu Lys His Leu Lys Ile	
205 210 215	
aag gtg gag gag ctg gag aac gag cgg aac cag tat gag tgg gag ctg	846
Lys Val Glu Glu Leu Glu Asn Glu Arg Asn Gln Tyr Glu Trp Glu Leu	
220 225 230	
aag gcc acc aag gct gag gta gcc cag ctg caa gaa cag gtg gcc cta	894
Lys Ala Thr Lys Ala Glu Val Ala Gln Leu Gln Glu Gln Val Ala Leu	
235 240 245	
aaa gat gca gaa att gag cgt ctc cac agc cag ctc tcc cgg agt gca	942
Lys Asp Ala Glu Ile Glu Arg Leu His Ser Gln Leu Ser Arg Ser Ala	
250 255 260 265	
gct ctc cac agc gac cat gca gag cga gat caa gaa atc cac cgt ctg	990
Ala Leu His Ser Asp His Ala Glu Arg Asp Gln Glu Ile His Arg Leu	
270 275 280	
aaa atg ggg atg gaa aca ctg ctg gtt gcc aat gag gat aag gac cgt	1038
Lys Met Gly Met Glu Thr Leu Leu Val Ala Asn Glu Asp Lys Asp Arg	
285 290 295	
cgg ata gag gag ctg aca ggg ctg ttg aac aag tac cta agg gta aag	1086
Arg Ile Glu Glu Leu Thr Gly Leu Leu Asn Lys Tyr Leu Arg Val Lys	
300 305 310	
gag att gtg atg gca act cag ggg cct tca gaa aga acc ctc tcc atc	1134
Glu Ile Val Met Ala Thr Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile	

315

320

325

aat gaa gat gaa ata gag gga agc ttc cga aaa tgg aat acc aca aat			1182
Asn Glu Asp Glu Ile Glu Gly Ser Phe Arg Lys Trp Asn Thr Thr Asn			
330	335	340	345
aaa agc cca gag gaa gtc ccg aag caa gag ata tca cca cga tgc agc			1230
Lys Ser Pro Glu Glu Val Pro Lys Gln Glu Ile Ser Pro Arg Cys Ser			
350	355	360	
tct ccc acc cca gga cca cct cct ttg cca cag aaa tca ctg gag agc			1278
Ser Pro Thr Pro Gly Pro Pro Leu Pro Gln Lys Ser Leu Glu Ser			
365	370	375	
agg gct cag aag aaa ctc tcc tgc agt cta gaa gac ttg aga cgt gaa			1326
Arg Ala Gln Lys Lys Leu Ser Cys Ser Leu Glu Asp Leu Arg Arg Glu			
380	385	390	
tct ggg gat aag tgt gtc gat ggg aac cag ctg tcc cca gtg gga gag			1374
Ser Gly Asp Lys Cys Val Asp Gly Asn Gln Leu Ser Pro Val Gly Glu			
395	400	405	
ccc aag gac agc tct ttc cta gcg gag cag aaa tac ccc aca tta cct			1422
Pro Lys Asp Ser Ser Phe Leu Ala Glu Gln Lys Tyr Pro Thr Leu Pro			
410	415	420	425
ggg aag ctt tca gga gcc aca ccc aat gga gaa gct gcc aaa tct cct			1470
Gly Lys Leu Ser Gly Ala Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro			
430	435	440	
ccc act gcc tcc ctc cag cct gac tct tca ggg agc agc cag cca aag			1518
Pro Thr Ala Ser Leu Gln Pro Asp Ser Ser Gly Ser Ser Gln Pro Lys			
445	450	455	
ctg aga gac aca gaa gga ggc tgg gaa gat ata gtc tca tct gct tcg			1566
Leu Arg Asp Thr Glu Gly Gly Trp Glu Asp Ile Val Ser Ser Ala Ser			
460	465	470	
tct ggg act gag tca agc cct cag tct ccc gtg aca cca gat ggc aaa			1614
Ser Gly Thr Glu Ser Ser Pro Gln Ser Pro Val Thr Pro Asp Gly Lys			
475	480	485	
cgg agc ccc aaa ggc att aag aag ttc tgg gga aag atc cga aga act			1662
Arg Ser Pro Lys Gly Ile Lys Lys Phe Trp Gly Lys Ile Arg Arg Thr			
490	495	500	505
cag tct gga aac ttc aat act gat gca ccg ggg atg gca gag ttt cga			1710
Gln Ser Gly Asn Phe Asn Thr Asp Ala Pro Gly Met Ala Glu Phe Arg			
510	515	520	
cga ggt ggg ctc cga gca act gcg gga cca agg ctt tct agg acc agg			1758
Arg Gly Gly Leu Arg Ala Thr Ala Gly Pro Arg Leu Ser Arg Thr Arg			
525	530	535	
gac acc aag gga cag aaa tgt gat gcc aat gcc ccc ttt gcc cag tgg			1806
Asp Thr Lys Gly Gln Lys Cys Asp Ala Asn Ala Pro Phe Ala Gln Trp			
540	545	550	
agc aca gaa cgc gta tgt aca tgg atg gag gat ttc ggc ctg ggt cag			1854
Ser Thr Glu Arg Val Cys Thr Trp Met Glu Asp Phe Gly Leu Gly Gln			

555

560

565

tat gtg atc ttt gcc aga cag tgg gtg aca tct gga cat aca cta ctg	570	575	580	585	1902
Tyr Val Ile Phe Ala Arg Gln Trp Val Thr Ser Gly His Thr Leu Leu					
aca gct acc cct cag gac atg gaa aag gag cta ggg att aaa cac ccc	590	595	600		1950
Thr Ala Thr Pro Gln Asp Met Glu Lys Glu Leu Gly Ile Lys His Pro					
ctc cac agg aag ctg gtt tta gca gtg aaa gct atc aac gcc aag	605	610	615		1998
Leu His Arg Lys Lys Leu Val Leu Ala Val Lys Ala Ile Asn Ala Lys					
caa gaa gaa acg tct gcg ctg ctg gac cac att tgg gtg aca cgg tgg	620	625	630		2046
Gln Glu Thr Ser Ala Leu Leu Asp His Ile Trp Val Thr Arg Trp					
ctt gat gat att ggc tta ccc caa tac aaa gac cag ttt cat gaa tca	635	640	645		2094
Leu Asp Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu Ser					
aga gtt gat ggg cga atg ctg caa tac cta act gtg aat gat cta ctc	650	655	660	665	2142
Arg Val Asp Gly Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu Leu					
ttc tta aaa gtc acc agc caa cta cat cat ctc agc atc aaa tgt gct	670	675	680		2190
Phe Leu Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys Ala					
att cac gtg cta cat gtc aac aag ttc aac ccc aac tgc ctg cac agg	685	690	695		2238
Ile His Val Leu His Val Asn Lys Phe Asn Pro Asn Cys Leu His Arg					
agg cct gct gat gag agt aac ctt tcc cct tcc gaa gtt gtg cag tgg	700	705	710		2286
Arg Pro Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln Trp					
tcc aac cac agg gta atg gag tgg ctg cga tcc gtg gac ctg gca gag	715	720	725		2334
Ser Asn His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala Glu					
tat gca ccc aac ctt cga ggg agt ggc gtc cat ggc ggc ctc att atc	730	735	740	745	2382
Tyr Ala Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile Ile					
ctg gag cct cgc ttt act ggg gac acc ctg gct atg ctt ctt aac atc	750	755	760		2430
Leu Glu Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn Ile					
ccc cca cag aag acg ctc ctc agg cgc cat ctg acc acc aag ttc aac	765	770	775		2478
Pro Pro Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe Asn					
gcc ctg att ggt cct gag gct gaa cag gaa aag cga gac aaa atg gcc	780	785	790		2526
Ala Leu Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Asp Lys Met Ala					
tca ccc gcc tac aca cct ctg acc acc acc gcc aaa gtt cgg cct agg	785	790			2574
Ser Pro Ala Tyr Thr Pro Leu Thr Thr Ala Lys Val Arg Pro Arg					

795	800	805	
aaa ctt gga ttt tca cat ttt gga aac atg aga aaa aag aag ttt gat Lys Leu Gly Phe Ser His Phe Gly Asn Met Arg Lys Lys Lys Phe Asp 810 815 820 825			2622
gaa tct aca gat tac att tgc ccc atg gag cct gga gat gct gtc agt Glu Ser Thr Asp Tyr Ile Cys Pro Met Glu Pro Gly Asp Ala Val Ser 830 835 840			2670
gac agc cac agg gtc tac gga gtc tac cgg ggc ctc agt ccc ctt gac Asp Ser His Arg Val Tyr Gly Val Tyr Arg Gly Leu Ser Pro Leu Asp 845 850 855			2718
aac cat gaa cta gat ggt ttg gac cag gtg gga cag ata agc tga Asn His Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser 860 865 870			2763
tgaccctgtt atctgccttc tctgtgcacg gagagctcac agtaacactg tgtgtcacca			2823
cgtaactgca cttcaccctc gtcctttgc atgatctaca gaaaacaatt gtgtcttgg			2883
gctggtctca ctacacactt taaggatggt cagaatatgc agttatacag ccacaaaggg			2943
gacagacttt gggaaactat agccaaatgt ggactctggg aaaacacctg cagacattag			3003
tagatgttta gtaattcata gtatccatgt ttcagcttga aacacatgag cagagggcag			3063
gccctggta atcgcaaaag gttcagttct cagacgctgc ccctattctt cagtcgaggg			3123
aagaattcaa gtgccttagg tttgtgagcc acaaagtctt ggctgagatc aaagtgccaa			3183
cagcggatgt ttggaccata gtgacaatgt aatttgattt taccttacta tagagtggcc			3243
acttgtttct gataataaaa acaatattta tgt			3276
<p><210> 20 <211> 871 <212> PRT <213> Mouse</p> <p><400> 20</p>			
Met Thr Ser Gly Ala Ser His Met Leu Glu Ala Ala Leu Glu Gln Met 1 5 10 15			
Asp Gly Ile Ile Ala Gly Thr Lys Thr Ala Ala Asp Phe Ser Asp Gly 20 25 30			
Thr Cys Glu Pro Gly Leu Ser Pro Pro Ser Thr Cys Leu Asn Ser Met 35 40 45			
Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu 50 55 60			

Ala Leu Pro Gln Glu Arg Glu Ala Leu Leu Ser Gln Val Pro Gly Pro
65 70 75 80

Thr Ala Thr Tyr Ile Lys Glu Trp Phe Glu Asp Ser Leu Ser Gln Val
85 90 95

Asn His His Gly Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
130 135 140

Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu Glu Met Leu
145 150 155 160

Gln Gln Glu Leu Leu Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp
165 170 175

Leu Met Thr Glu Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu
180 185 190

Lys Glu Gln Lys Glu Gln Glu Glu Lys Gln Arg Lys Ala Glu Glu Leu
195 200 205

Leu Gln Glu Leu Lys His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn
210 215 220

Glu Arg Asn Gln Tyr Glu Trp Glu Leu Lys Ala Thr Lys Ala Glu Val
225 230 235 240

Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu Arg
245 250 255

Leu His Ser Gln Leu Ser Arg Ser Ala Ala Leu His Ser Asp His Ala
260 265 270

Glu Arg Asp Gln Glu Ile His Arg Leu Lys Met Gly Met Glu Thr Leu
275 280 285

Leu Val Ala Asn Glu Asp Lys Asp Arg Arg Ile Glu Glu Leu Thr Gly
290 295 300

Leu Leu Asn Lys Tyr Leu Arg Val Lys Glu Ile Val Met Ala Thr Gln
305 310 315 320

Gly Pro Ser Glu Arg Thr Leu Ser Ile Asn Glu Asp Glu Ile Glu Gly
325 330 335

Ser Phe Arg Lys Trp Asn Thr Thr Asn Lys Ser Pro Glu Glu Val Pro
340 345 350

Lys Gln Glu Ile Ser Pro Arg Cys Ser Ser Pro Thr Pro Gly Pro Pro
355 360 365

Pro Leu Pro Gln Lys Ser Leu Glu Ser Arg Ala Gln Lys Lys Leu Ser
370 375 380

Cys Ser Leu Glu Asp Leu Arg Arg Glu Ser Gly Asp Lys Cys Val Asp
385 390 395 400

Gly Asn Gln Leu Ser Pro Val Gly Glu Pro Lys Asp Ser Ser Phe Leu
405 410 415

Ala Glu Gln Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala Thr
420 425 430

Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ala Ser Leu Gln Pro
435 440 445

Asp Ser Ser Gly Ser Ser Gln Pro Lys Leu Arg Asp Thr Glu Gly Gly
450 455 460

Trp Glu Asp Ile Val Ser Ser Ala Ser Ser Gly Thr Glu Ser Ser Pro
465 470 475 480

Gln Ser Pro Val Thr Pro Asp Gly Lys Arg Ser Pro Lys Gly Ile Lys
485 490 495

Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser Gly Asn Phe Asn Thr
500 505 510

Asp Ala Pro Gly Met Ala Glu Phe Arg Arg Gly Gly Leu Arg Ala Thr
515 520 525

Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Thr Lys Gly Gln Lys Cys
530 535 540

Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr Glu Arg Val Cys Thr
545 550 555 560

Trp Met Glu Asp Phe Gly Leu Gly Gln Tyr Val Ile Phe Ala Arg Gln
565 570 575

Trp Val Thr Ser Gly His Thr Leu Leu Thr Ala Thr Pro Gln Asp Met
580 585 590

Glu Lys Glu Leu Gly Ile Lys His Pro Leu His Arg Lys Lys Leu Val
595 600 605

Leu Ala Val Lys Ala Ile Asn Ala Lys Gln Glu Glu Thr Ser Ala Leu
610 615 620

Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp Asp Ile Gly Leu Pro
625 630 635 640

Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val Asp Gly Arg Met Leu
645 650 655

Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu Lys Val Thr Ser Gln
660 665 670

Leu His His Leu Ser Ile Lys Cys Ala Ile His Val Leu His Val Asn
675 680 685

Lys Phe Asn Pro Asn Cys Leu His Arg Arg Pro Ala Asp Glu Ser Asn
690 695 700

Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn His Arg Val Met Glu
705 710 715 720

Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala Pro Asn Leu Arg Gly
725 730 735

Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu Pro Arg Phe Thr Gly
740 745 750

Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro Gln Lys Thr Leu Leu
755 760 765

Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu Ile Gly Pro Glu Ala
770 775 780

Glu Gln Glu Lys Arg Asp Lys Met Ala Ser Pro Ala Tyr Thr Pro Leu
785 790 795 800

Thr Thr Thr Ala Lys Val Arg Pro Arg Lys Leu Gly Phe Ser His Phe
805 810 815

Gly Asn Met Arg Lys Lys Phe Asp Glu Ser Thr Asp Tyr Ile Cys
820 825 830

Pro Met Glu Pro Gly Asp Ala Val Ser Asp Ser His Arg Val Tyr Gly
835 840 845

Val Tyr Arg Gly Leu Ser Pro Leu Asp Asn His Glu Leu Asp Gly Leu
850 855 860

Asp Gln Val Gly Gln Ile Ser
865 870

<210> 21
<211> 5020
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (174)...(1277)

<400> 21
tgcaggcata gtctgttggc ctgacgtcag atgtcgcttt gacaaacgcc cccggggct 60

gaggaaggct ctccgctgct ctgatgggcc agcccagtcg tggcccaagct ccctggagag 120
gcattccgcat cctctggct gagccgttagc tcctgtgacg ctgacttcca ggc atg 176
Met
1

agg tgg ctc ctg ccc tgg acg ctg gca gcc gtg gca gtc ctg agg gtg 224
Arg Trp Leu Leu Pro Trp Thr Leu Ala Ala Val Ala Val Leu Arg Val
5 10 15

ggc aac atc ctg gcc acg gcc ctc tct cca acc ccc aca aca atg acc 272
Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Met Thr
20 25 30

ttc acc cca gca cca cta gag gaa acg act aca cgc ccc gaa ttc tgc 320
Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Arg Pro Glu Phe Cys
35 40 45

aag tgg cca tgt gag tgc cca caa tcc cca cct cgc tgc cca ctg ggc 368
Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu Gly
50 55 60 65

gtc agc cta atc aca gat ggc tgt gaa tgc tgt aag ata tgt gcc cag 416

Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala Gln			
70	75	80	
cag ctt ggg gac aac tgc aca gag gct gcc atc tgt gac cca cac cgg			464
Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His Arg			
85	90	95	
ggc ctc tac tgc gat tac agt ggg gat cgc ccg agg tac gca ata gga			512
Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile Gly			
100	105	110	
gtg tgt gca cag gtg gtc ggt gtg ggc tgt gtc ctg gat ggc gta cgc			560
Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val Arg			
115	120	125	
tac acc aat ggc gag tcc ttc caa ccc aac tgc agg tac aac tgt acc			608
Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys Thr			
130	135	140	145
tgc att gat ggc acg gtg ggc tgc aca ccg ctg tgc cta agc ccc agg			656
Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro Arg			
150	155	160	
ccc cca cgc ctc tgg tgc cgc cag ccc ccg cac gtg aga gtc cct ggc			704
Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro Gly			
165	170	175	
cag tgc tgt gag cag tgg gtg tgt gat gat gac gca agg aga cca cgc			752
Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Ala Arg Arg Pro Arg			
180	185	190	
cag act gca ctg ttg gac acc aga gcc ttt gca gcg tca ggc gcc gtg			800
Gln Thr Ala Leu Leu Asp Thr Arg Ala Phe Ala Ala Ser Gly Ala Val			
195	200	205	
gag caa cgg tat gag aac tgc ata gcc tac act agt ccc tgg agc ccc			848
Glu Gln Arg Tyr Glu Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser Pro			
210	215	220	225
tgc tct acc acc tgt ggc cta ggt atc tcc act ccg atc tct aac gtc			896
Cys Ser Thr Thr Cys Gly Leu Gly Ile Ser Thr Arg Ile Ser Asn Val			
230	235	240	
aat gcc cgg tgc tgg cca gag cag gaa agt cgc ctc tgc aac ctg cgg			944
Asn Ala Arg Cys Trp Pro Glu Gln Ser Arg Leu Cys Asn Leu Arg			
245	250	255	
cca tgt gat gtg gac atc caa cta cac atc aag gca ggg aag aaa tgc			992
Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys Cys			
260	265	270	
ctg gct gtg tac cag cca gag gag gcc acg aac ttc act ctc gca ggc			1040
Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala Gly			
275	280	285	
tgt gtc agc aca cgc acc tac cga ccc aag tac tgc gga gtc tgt act			1088
Cys Val Ser Thr Arg Thr Tyr Arg Pro Lys Tyr Cys Gly Val Cys Thr			
290	295	300	305
gac aat agg tgt tgc atc ccc tac aag tcc aag acc atc agt gtg gat			1136

Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val Asp		
310	315	320
ttc cag tgt cca gag ggg cca ggt ttc tcc cgg cag gtc cta tgg att		1184
Phe Gln Cys Pro Glu Gly Pro Gly Phe Ser Arg Gln Val Leu Trp Ile		
325	330	335
aat gct tgc ttc tgc aac ctg agc tgc agg aat cct aac gat atc ttt		1232
Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile Phe		
340	345	350
gct gac ttg gaa tct tac cct gac ttc gaa gag att gcc aat tag		1277
Ala Asp Leu Glu Ser Tyr Pro Asp Phe Glu Glu Ile Ala Asn		
355	360	365
gtgggtgtgt ggctcagggt aaagttccat gctgcaaagc agccagccct ttgtggtcca		1337
ggacttcaca attgagcctt atttcatcta cttcctactc gattctgaat tcccagtttc		1397
tgttcctgtt ttgacaatcg taatggccca ggagagtgc gctcaggctc agacaatggg		1457
ttcctccttg gggacattct acatcattcc aaggaaaaca catctctgac tgttcacaat		1517
ggaagcaaag cctggcccag ctagtctggc tccagcctgg gcaagttgtc agaagttgt		1577
atgggattgt ccaaggaaaa gcatcagctg aagaaccagt atcatgaagt ctttcctcag		1637
atgccaagcc tagggatgct gggatccctt cagacagatg gatgggattg gggacacagg		1697
aataagctat tattttaccc ttgccaaatg atactatcct ggttatttct gcctaaaaca		1757
tacccaaagt gttctgttc cactgatctg tatatcaca gtcaccaaac attttccagg		1817
tgaggaccat agttgtgtca ttctgtttt ctattgaaaa tcattttaaa aagaaggaaa		1877
aaaaaaaaaaa gaaaagaaaa gaaagtcat tcattaactt gggcacttcc tcctctcacc		1937
ccatattcta taaagggcta aacttgggtt ctgttgcattc aggaatgtaa tttgagaagt		1997
cttacttttg cagggagatg gtagccctca attcatcccg tagatggac aaggccagcc		2057
aatcttcaa gccatagctg ggcaggtcac tgaatctgct gctggccaag ttcttaggac		2117
aattagccaa aatctggcc tctctctccc tagggttcat gggagtttgtt agggaccgta		2177
gagtgacttg tctgttgtct caaaaagtaa gatggaaaga tttctcatg gcccattaa		2237
gactcttttg aagtctacgc cagacctaac agaataatgtg catcaaacaa acaagtggat		2297
caccctccca tggcctgggt gacctctagc agtcacccag tgactgttgtt aaggccacag		2357
tagtccctgg acccaggaca aatctttttt gttcagtga cctactttac agcctcagtg		2417
tctatgaaga aagttaactc agtttctca tctgaagaca gaagtcgacc agccattcag		2477
aaatggggat ctatttagta gtggtaaacg ttaaagagtt tgtaagctaa agaaatattt		2537
ttttcctaa gtgataatga ggttgttacc tatttttagag gtagaatttt ctgtcatcat		2597
ccttttattt gtttctacat actacccatt gttctcaata tttgccacac atttactcat		2657

tgaaacttgc tgataacaca gaggacttcc cttaatgatt tctgttcttg acactgtgaa	2717
atatcaattc aaagaggcta ataagttcaa tcaaagtcac ctatctgaag actcatagcc	2777
agagaagatt gccttcataat ttccccttg cttctggacc ttgtaaacat gtcagggcag	2837
gaaagcatac agaagtcagc agcttgcctt cttagtattt gctctctagc cccttcacg	2897
taaggaggaa gtgtgtctag gtactaagga tccaaacctaa actggacaga aaagggcatg	2957
tgcattatcc cctgtggctc ctcctgcctt ggaatcagaa ctagcttaca gcatgcttt	3017
atatgatgat tcagtttgc ccacaccata cataatggca tatggagaa ctatacacac	3077
actcataaaat ggatttgtaa gtaggaaagg ggacttgaga tttcccctcc ttccctgcaac	3137
ttcccaaagg cctggcctta tgcaaggcaa acagtggtgc ttaagatgta tttgggaaag	3197
aaaatactat atatataatat tcctattttt ccttagaagc cttttcttcc aggtatctcat	3257
cttaacagta agaaatcctc tcttaagaga ggcttagtat tttgagtaaaa cataatgttca	3317
tatgtgtaca agtacttgta tgtaaatata agtaccact gtgggttatt aattaggtaa	3377
attttatgtg gtatcatatt tgattttctt ctattggaaa aatctgcctt aacagctaacc	3437
tctgtaaagaa cttccatagg agccataagc tagggcttc ccaggtatcc atccttttt	3497
gggaaactga gctgagcatc ttcaacccaa ggagtttaggg tgatcattgg gaataggaga	3557
aaggatggc cagggtagct ccatcgat ttagaaacag acctggcata cagaacgacc	3617
agaggaacca accttcttgc aaccaaggaa aaaagacttg gatgtatata atagaagctt	3677
tttctaatacg tcagaaacag actttaattt gatggctgg ttcaaggaaa gttaagaatg	3737
tccattatcg ttaaaaacaa aagtccat ttagatagctt atttggtgct aagccctacg	3797
gtgcatttttgc tccggctatc acttagcaga gccatgctca gtacacagtc tttctctatt	3857
caataatacg aaacgctgaa gctcaaaggc actgaggagc tgaggctcag aagcatgttt	3917
agtccactct atcaggggggg gaagagatct tgacggaacc taaatgacta ctattggaaa	3977
ctcatatttgc aaagcttca gaagtccac ccccacccca tccccagatg cttagaaact	4037
aaagaagcaa tgaggatgag ctgccttca gtgaagaggt tcactactgc accaagagtg	4097
aatgtcttag gtgtacttag tcattggaca gggagacctg agtgagttt gtaacctgca	4157
gcttactaaa ctttacaatg agcatttggaa gagccaagac tgcttctcg cgcttactg	4217
acatggcttgc cttaatcttc tcagtggacc caagagtcag ggcgttacca ctgcccattt	4277
tagggctgag aaagcaaaat ctccaggagt taagtgattt gctcaagttt ttaaccaacc	4337
gaggcactgc agataaactc cgaagccag tgcgtatgaa catgcccattg ccatctctcc	4397
ggacacgcag cccattttcc tgttcctaaa ccaaaggctc agagtcacca gaaccaactc	4457

acaggacagt gcagaaaattc taatgtcgag ggtgattaga gactgatcaa agaaagtaat 4517
ttcaaatgat atgattgttt gtaagcaccc tagttaattc tggactacat atgcataag 4577
attgtgaaga acattacagc ctgtgactat aacgttgact tctgtcattt cttttaaag 4637
acttggtttt ttttttact caaaggaccc acagtgacag ccctgaatgg ttgagaagca 4697
ttgattagct gtgagtcctg catatgtatg tatgtgtgtg tgtgtgtgtg tatttgtatg 4757
tacttatcta ttttcaaact gtgattgtgt atttaaatat tcctcctgcc attttctaag 4817
tgattacgca taaagaaaaca ccttgaatg tcctaataaa ggagagctag cccttggcg 4877
gcctgtcaca ttttgcaca ttcctcattt ttctcatgat ctgtgttagca gggaatgtgt 4937
ttgttcaacc atgatgagtt ttcattgttc aaattctttg tttacagctt ttctccttaa 4997
agcaataaat catcagcaac agt 5020

<210> 22
<211> 367
<212> PRT
<213> Mouse

<400> 22

Met Arg Trp Leu Leu Pro Trp Thr Leu Ala Ala Val Ala Val Leu Arg
1 5 10 15

Val Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Thr Met
20 25 30

Thr Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Thr Arg Pro Glu Phe
35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu
50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala
65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
115 120 125

Arg Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys
130 135 140

Thr Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro
145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro
165 170 175

Gly Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Asp Ala Arg Arg Pro
180 185 190

Arg Gln Thr Ala Leu Leu Asp Thr Arg Ala Phe Ala Ala Ser Gly Ala
195 200 205

Val Glu Gln Arg Tyr Glu Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
210 215 220

Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ser Thr Arg Ile Ser Asn
225 230 235 240

Val Asn Ala Arg Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
245 250 255

Arg Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys
260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala
275 280 285

Gly Cys Val Ser Thr Arg Thr Tyr Arg Pro Lys Tyr Cys Gly Val Cys
290 295 300

Thr Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val
305 310 315 320

Asp Phe Gln Cys Pro Glu Gly Pro Gly Phe Ser Arg Gln Val Leu Trp
325 330 335

Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
340 345 350

Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Glu Glu Ile Ala Asn
355 360 365

<210> 23
<211> 1580
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (318) .. (794)

<400> 23		
ctgagaagga aaccgcacatct tcagacttct gctcaactcac gagaggagct agggtcacatcg	60	
gaccgcataag atcctttcac atcgctccga ctcgcccggaa cactcctcac cagttccctc	120	
agccacagcc ctacccgtga gctccggact tccccggctt tctgtggatg ctcaggcaga	180	
ctgcagagac ctagcctagg acagcagtga gggggacact cctctccctct cctctccctct	240	
ggtatcagcg tctcccccaa gggggacgag catggtgatt gtgccttgaa ggaccttggc	300	
tctggatgtc tgagaag atg ctg gtc atg aag ctg ttc act tgc ttc tta	350	
Met Leu Val Met Lys Leu Phe Thr Cys Phe Leu		
1 5 10		
cag gtc cta gct ggg ttg gct gtg cat tcc cag ggg gcc ctg tct gct	398	
Gln Val Leu Ala Gly Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala		
15 20 25		
ggg aac aac tca aca gaa gtg gaa gtg gtg cct ttc aac gaa gtg tgg	446	
Gly Asn Asn Ser Thr Glu Val Glu Val Val Pro Phe Asn Glu Val Trp		
30 35 40		
ggt cgc agc tac tgt cgg ccc atg gag aag ctg gtg tac atc ttg gat	494	
Gly Arg Ser Tyr Cys Arg Pro Met Glu Lys Leu Val Tyr Ile Leu Asp		
45 50 55		
gaa tac cct gat gag gtg tct cac ata ttc agt ccg tcc tgt gtc ctt	542	
Glu Tyr Pro Asp Glu Val Ser His Ile Phe Ser Pro Ser Cys Val Leu		
60 65 70 75		
ctg agt cgc tgt agt ggc tgc tgt ggt gat gaa ggt ctg cac tgt gtg	590	
Leu Ser Arg Cys Ser Gly Cys Gly Asp Glu Gly Leu His Cys Val		
80 85 90		
ccg ata aag aca gcc aac atc act atg cag atc ttg aag att ccc ccc	638	
Pro Ile Lys Thr Ala Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro		
95 100 105		
aat cgg gat cca cat ttc tat gtg gag atg aca ttt tct cag gat gtg	686	
Asn Arg Asp Pro His Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val		
110 115 120		
ctc tgt gaa tgc aga cct att ctg gag acg aca aag gca gaa agg agg	734	
Leu Cys Glu Cys Arg Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg		
125 130 135		
aaa acc aag ggg aag agg aag agg agt aga aac tca cag act gag gaa	782	
Lys Thr Lys Gly Lys Arg Lys Arg Ser Arg Asn Ser Gln Thr Glu Glu		

140	145	150	155	
ccc cac ccg tga tgtcatttcc	cgaggtaac cagccactca	gaggagagcc		834
Pro His Pro				

ccacacccag ctcacgtatt tattaccgtc	accctctcag aaccctccct	gctggtaacct	894
accctctatt tattagccga ctcgtccctg	ctgaatgacg tgccccctcc	aagataaggg	954
gcatggaagg acaagacgct caggaattca	gtgccttaaa acagaacgag	agagaaagaa	1014
agaagccagc cacggatctg tggagcttc	ggcttggaa gaagcaagac	atggacatgg	1074
ccttacaagg ggcaagccgc	accccagagg ccctggctct	ccagggact ggagaagaga	1134
agaggaggcc tagaacctgc	cctgattccc agctccaccc	agagagcagc tctggcccg	1194
gctgcattga aggcatgtag	aggggaccca gtctactgta	tcctggagat gggacaggac	1254
attcggctct ggagagcaga	gcttcctgt ggagttgcc	cttcagccta gaagtttatg	1314
cttcaccctt tgcaaaggc	cttgcaccc tctctggAAC	acaggcagag tggcctgggg	1374
ctgagcagag ggcaggctgg	aggagcagta gcccgtggac	tttgaccgat acaagtctgg	1434
gttgtgtgtc ttctgtgtac	agctacggga agtgagccga	ctcctggagg gcccggcag	1494
cccacccgtt gtctctgccg	ggactaactg ccaagccaga	ttctcttcaa taaagcattc	1554
tagtctggaa aaaaaaaaaa			1580

<210> 24
<211> 158
<212> PRT
<213> Mouse

<400> 24

Met Leu Val Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
1 5 10 15

Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
20 25 30

Glu Val Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
35 40 45

Arg Pro Met Glu Lys Leu Val Tyr Ile Leu Asp Glu Tyr Pro Asp Glu
50 55 60

Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
65 70 75 80

Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Pro Ile Lys Thr Ala
85 90 95

Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
100 105 110

Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
115 120 125

Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
130 135 140

Arg Lys Arg Ser Arg Asn Ser Gln Thr Glu Glu Pro His Pro
145 150 155

<210> 25
<211> 2879
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (223)...(2124)

<400> 25
ggcacgaggg ccacccgagt cgccggcgtc gccacctgca cttggctctg gaccccccgcg 60
gacagagccc cggccggccg ccgcttcccg ccgcctgccc tgcccacctg ccaggtattta 120
ccacttaaag aaaccctttt accggcaaac ctatgctaaa gagtataagt aacaaaggaa 180
accaaacagt tatctgtcaa gtaacaagca ttatgaca ga atg gct cac ctt 234
Met Ala His Leu
1
aag cga cta gta aaa ttg cac att aaa aga cat tac cac aga aag ttc 282
Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr His Arg Lys Phe
5 10 15 20
tgg aag ctg ggt gca gtc atc ttt ttc ttt tta gta gtt ctg att tta 330
Trp Lys Leu Gly Ala Val Ile Phe Phe Leu Val Val Leu Ile Leu
25 30 35
atg caa aga gaa gta agt gtt cag tat tcc aag gag gaa tca aag atg 378
Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu Glu Ser Lys Met
40 45 50
gag agg aac ttg aaa aac aaa aac aaa atg ttg gat ttt atg ctc gaa 426
Glu Arg Asn Leu Lys Asn Lys Asn Lys Met Leu Asp Phe Met Leu Glu
55 60 65
gct gta aat aat att aaa gat gca atg cca aag atg caa ata gga gcg 474
Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met Gln Ile Gly Ala
70 75 80

ccc att aag gag aat atc gac gtc cgc gag aga ccc tgt ctg caa ggg Pro Ile Lys Glu Asn Ile Asp Val Arg Glu Arg Pro Cys Leu Gln Gly 85 90 95 100	522
tac tac aca gcc gcg gag ttg aag ccg gtt ttt gat cgc cca cct cag Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Phe Asp Arg Pro Pro Gln 105 110 115	570
gat tct aac gca cct ggt gct tct ggc aag ccg ttt aag atc acc cac Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Pro Phe Lys Ile Thr His 120 125 130	618
ctc agc ccg gag gag cag aag gag aaa gag cga ggg gaa acg aag cac Leu Ser Pro Glu Glu Gln Lys Glu Lys Glu Arg Gly Glu Thr Lys His 135 140 145	666
tgc ttc aac gcc ttt gca agt gac aga att tct ctg cac cgg gac ctt Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu His Arg Asp Leu 150 155 160	714
ggg cct gac acc cga cca cct gaa tgt att gaa caa aaa ttt aag cgc Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln Lys Phe Lys Arg 165 170 175 180	762
tgc ccg ccc ctg cct acc acc agt gtc ata ata gtc ttt cac aat gaa Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val Phe His Asn Glu 185 190 195	810
gca tgg tcc acg ctg ctt agg acc gtc cac agt gtg ctc tat tct tca Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Leu Tyr Ser Ser 200 205 210	858
cct gcc ata ctg ctg aag gag atc att ttg gtg gat gat gct agt gta Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Val 215 220 225	906
gac gac tac ctg cat gaa aag ctg gag gaa tac ata aaa cag ttt tct Asp Asp Tyr Leu His Glu Lys Leu Glu Glu Tyr Ile Lys Gln Phe Ser 230 235 240	954
att gtg aaa ata gtc agg cag caa gaa agg aaa ggc ctg atc acc gcg Ile Val Lys Ile Val Arg Gln Gln Glu Arg Lys Gly Leu Ile Thr Ala 245 250 255 260	1002
cgg ttg cta ggg gca gct gta gca act gcc gag acg ctc acg ttc tta Arg Leu Leu Gly Ala Ala Val Ala Thr Ala Glu Thr Leu Thr Phe Leu 265 270 275	1050
gat gct cac tgt gag tgc ttc tat ggc tgg ctg gaa cct ctg ctg gcc Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu Pro Leu Leu Ala 280 285 290	1098
agg ata gct gag aac tac act gcc gtg gtg agt cca gac atc gca tcc Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro Asp Ile Ala Ser 295 300 305	1146
ata gat cta aac aca ttt gaa ttc aac aag cct tct ccg tac gga agc Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser Pro Tyr Gly Ser 310 315 320	1194

aac cat aac cgt gga aat ttt gac tgg agc ctt tcc ttt ggc tgg gag		1242
Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser Phe Gly Trp Glu		
325 330 335 340		
tca ctt cct gat cat gag aag caa aga agg aaa gat gaa acc tac cca		1290
Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp Glu Thr Tyr Pro		
345 350 355		
att aag acc ccc acc ttt gca gga ggc ctt ttt tct ata tct aaa aaa		1338
Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Lys		
360 365 370		
tat ttt gag cac att gga agt tac gat gaa gaa atg gaa atc tgg gga		1386
Tyr Phe Glu His Ile Gly Ser Tyr Asp Glu Glu Met Glu Ile Trp Gly		
375 380 385		
ggg gaa aat ata gaa atg tca ttc cga gtg tgg caa tgt ggt ggg cag		1434
Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln Cys Gly Gly Gln		
390 395 400		
ttg gag att atg cct tgc tct gtt gga cat gtt ttt cgc agc aaa		1482
Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val Phe Arg Ser Lys		
405 410 415 420		
agc cct cat acc ttc cca aaa ggc acg cag gtg att gct cgt aac caa		1530
Ser Pro His Thr Phe Pro Lys Gly Thr Gln Val Ile Ala Arg Asn Gln		
425 430 435		
gtt cgc ctt gca gag gtc tgg atg gac gaa tac aag gaa ata ttt tat		1578
Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys Glu Ile Phe Tyr		
440 445 450		
agg aga aac aca gat gca gca aaa atc gtt aag caa aaa tca ttt ggt		1626
Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln Lys Ser Phe Gly		
455 460 465		
gat ctt tcc aaa aga ttt gaa ata aag aaa cgc ctt cag tgt aaa aat		1674
Asp Leu Ser Lys Arg Phe Glu Ile Lys Lys Arg Leu Gln Cys Lys Asn		
470 475 480		
ttt acc tgg tac ctg aac act att tac ccg gaa ggc tat gtg cca gac		1722
Phe Thr Trp Tyr Leu Asn Thr Ile Tyr Pro Glu Ala Tyr Val Pro Asp		
485 490 495 500		
ctt aat cct gtt ata tct gga tat att aag agt gtg ggt caa cct tta		1770
Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val Gly Gln Pro Leu		
505 510 515		
tgt ctg gat gtt ggt gag aat aac cag gga ggc aaa cca ttg att ctg		1818
Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys Pro Leu Ile Leu		
520 525 530		
tac acg tgc cac ggc ctc ggg gga aat cag tac ttc gag tat tct gct		1866
Tyr Thr Cys His Gly Leu Gly Asn Gln Tyr Phe Glu Tyr Ser Ala		
535 540 545		
cag cgt gaa atc cgg cac aac atc cag aag gag ctg tgt ctt cat gct		1914
Gln Arg Glu Ile Arg His Asn Ile Gln Lys Glu Leu Cys Leu His Ala		
550 555 560		

act cag ggt gtc gtc cag ctg aag gca tgt gtc tat aaa ggt cac agg	1962
Thr Gln Gly Val Val Gln Leu Lys Ala Cys Val Tyr Lys Gly His Arg	
565 570 575 580	
acc atc gcc cct gga gaa cag ata tgg gag att cggtt gac caa ctt	2010
Thr Ile Ala Pro Gly Glu Gln Ile Trp Glu Ile Arg Lys Asp Gln Leu	
585 590 595	
ctat tat aat cca tta ttt aaa atg tgc ctt tca tca aat gga gag cat	2058
Leu Tyr Asn Pro Leu Phe Lys Met Cys Leu Ser Ser Asn Gly Glu His	
600 605 610	
ccaa aac tta gtg cca tgt gac gca aca gat cta ctc caa aaa tgg att	2106
Pro Asn Leu Val Pro Cys Asp Ala Thr Asp Leu Leu Gln Lys Trp Ile	
615 620 625	
ttt agc caa aat gaa taa gtgttcctta aaattaagga gttgaaaagg	2154
Phe Ser Gln Asn Glu	
630	
acatactctt cctcataaaa ctgtgactag gcatacactg tagttgtga aaattatgca	2214
aaagcagcta attgttaactt attccaagtg catttcctta tttatatctt aagatgtcta	2274
tgttagaaccg ctgcagaaac cctggggttt ctgtctgaaa gcacagcaac tagaatacca	2334
aagacgattc tgaaatgtcc agatgttagaa gagagatgtt tacagtgtga agaaaataat	2394
ttccttagta aagtgaggtg tgggtgtaca cttggggatc tacacacctg catccacaca	2454
ctcacagctg aaaatgtttt ccctaatttt agggcaata gaaaaagatt tgatactgta	2514
tttttataac tatatagaaa tggatcaatg aaggccagtc atttggcctt tcggtacaaa	2574
ccaggaactt ttatcgatc tagaattcat tgggtttaaa tccaggtaaa ctttgggtgt	2634
ctcttggta cttgtctgtc aaatattcc ttaaacatga agttgataag gagaggacta	2694
tttttaacat ttaaattttt ggaaaattta caaatatttt ttagaagccc actccacttg	2754
atgcacatga gtctccccca aatagtttt ctgaagtgac tatactgtgt gtttctcag	2814
agtactttt aaaaaataaa taaactttt aaattattag ctgtaaaaaa aaaaaaaaaa	2874
aaaaaa	2879

<210> 26
 <211> 633
 <212> PRT
 <213> Mouse

<400> 26

Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
 1 5 10 15

His Arg Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Leu Val

20

25

30

Val Leu Ile Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
35 40 45

Glu Ser Lys Met Glu Arg Asn Leu Lys Asn Lys Met Leu Asp
50 55 60

Phe Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
65 70 75 80

Gln Ile Gly Ala Pro Ile Lys Glu Asn Ile Asp Val Arg Glu Arg Pro
85 90 95

Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Phe Asp
100 105 110

Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Pro Phe
115 120 125

Lys Ile Thr His Leu Ser Pro Glu Glu Gln Lys Glu Lys Glu Arg Gly
130 135 140

Glu Thr Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
145 150 155 160

His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
165 170 175

Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
180 185 190

Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val
195 200 205

Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp
210 215 220

Asp Ala Ser Val Asp Asp Tyr Leu His Glu Lys Leu Glu Glu Tyr Ile
225 230 235 240

Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Gln Glu Arg Lys Gly
245 250 255

Leu Ile Thr Ala Arg Leu Leu Gly Ala Ala Val Ala Thr Ala Glu Thr

260

265

270

Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu
275 280 285

Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro
290 295 300

Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser
305 310 315 320

Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser
325 330 335

Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp
340 345 350

Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser
355 360 365

Ile Ser Lys Lys Tyr Phe Glu His Ile Gly Ser Tyr Asp Glu Glu Met
370 375 380

Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln
385 390 395 400

Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val
405 410 415

Phe Arg Ser Lys Ser Pro His Thr Phe Pro Lys Gly Thr Gln Val Ile
420 425 430

Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys
435 440 445

Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln
450 455 460

Lys Ser Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys Lys Arg Leu
465 470 475 480

Gln Cys Lys Asn Phe Thr Trp Tyr Leu Asn Thr Ile Tyr Pro Glu Ala
485 490 495

Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val

500

505

510

Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys
515 520 525

Pro Leu Ile Leu Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe
530 535 540

Glu Tyr Ser Ala Gln Arg Glu Ile Arg His Asn Ile Gln Lys Glu Leu
545 550 555 560

Cys Leu His Ala Thr Gln Gly Val Val Gln Leu Lys Ala Cys Val Tyr
565 570 575

Lys Gly His Arg Thr Ile Ala Pro Gly Glu Gln Ile Trp Glu Ile Arg
580 585 590

Lys Asp Gln Leu Leu Tyr Asn Pro Leu Phe Lys Met Cys Leu Ser Ser
595 600 605

Asn Gly Glu His Pro Asn Leu Val Pro Cys Asp Ala Thr Asp Leu Leu
610 615 620

Gln Lys Trp Ile Phe Ser Gln Asn Glu
625 630

<210> 27
<211> 5540
<212> DNA
<213> human

<220>
<221> CDS
<222> (144)..(1838)

<400> 27
aattgcttcc ggggagttgc gagggagcga gggggataa aggacccgcg aggaagggcc 60
cgcgatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtggaa ggagcggacc 120
ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gcc ctc ggc 173
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
1 5 10
atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
15 20 25
ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly

30

35

40

ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac	317
Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His	
45 50 55	
tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc	365
Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile	
60 65 70	
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca	413
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr	
75 80 85 90	
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta	461
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu	
95 100 105	
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa	509
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu	
110 115 120	
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg	557
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly	
125 130 135	
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat	605
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His	
140 145 150	
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat	653
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp	
155 160 165 170	
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca	701
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr	
175 180 185	
cag ctg gcc cg att gcg gac agt aag gat cat gtg ttt ccc gtg aat	749
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn	
190 195 200	
gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag	797
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys	
205 210 215	
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga	845
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly	
220 225 230	
gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc	893
Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg	
235 240 245 250	
aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca	941
Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr	
255 260 265	
ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca	989
Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro	

270	275	280	
gct cct atc tta aaa gaa gtt ggc atg aaa gct gca ctc cag gtc agc Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val Ser 285	290	295	1037
atg aac gat ggc ctc tct ttt atc tcc agt tct gtc atc atc acc acc Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr 300	305	310	1085
aca cac tgt tct gac ggt tcc atc ctg gcc atc gcc ctg ctg atc ctg Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu 315	320	325	1133
ttc ctg ctc cta gcc ctg gct ctc ctc tgg tgg ttc tgg ccc ctc tgc Phe Leu Leu Leu Ala Leu Leu Leu Trp Trp Phe Trp Pro Leu Cys 335	340	345	1181
tgc act gtg att atc aag gag gtc cct cca ccc cct gcc gag gag agt Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Pro Ala Glu Glu Ser 350	355	360	1229
gag gaa gaa gat gat gat ggt ctg cct aag aaa aag tgg cca acg gta Glu Glu Asp Asp Gly Leu Pro Lys Lys Lys Trp Pro Thr Val 365	370	375	1277
gac gcc tct tat tat ggt ggg aga ggc gtt gga ggc att aaa aga atg Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Ile Lys Arg Met 380	385	390	1325
gag gtt cgt tgg gga gaa aag ggc tcc aca gaa gaa ggt gct aag ttg Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu 395	400	405	1373
gaa aag gca aag aat gca aga gtc aag atg ccg gag cag gaa tat gaa Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr Glu 415	420	425	1421
ttc cct gag ccg cga aat ctc aac aac aat atg cgt cgg cct tct tcc Phe Pro Glu Pro Arg Asn Leu Asn Asn Asn Met Arg Arg Pro Ser Ser 430	435	440	1469
ccc cgg aag tgg tac tct cca atc aag gga aaa ctc gat gcc ttg tgg Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp 445	450	455	1517
gtc cta ctg agg aaa gga tat gat cgt gtg tct gtg atg cgt cca cag Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro Gln 460	465	470	1565
cca gga gac acg ggg cgc tgc atc aac ttc acc agg gtc aag aac aac Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn Asn 475	480	485	1613
cag cca gcc aag tac cca ctc aac aac gcc tac cac acc tcc tcg ccg Gln Pro Ala Lys Tyr Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro 495	500	505	1661
cct cct gcc ccc atc tac act ccc cca cct cct gcg ccc cac tgc cct Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Ala Pro His Cys Pro			1709

510	515	520	
ccc ccg ccc ccc agc gcc cct acc ccc atc ccg tcc cca cct tcc Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser	525	530	1757
		535	
acc ctt ccc cct ccc cag gct cca cct ccc aac agg gca cct cct Thr Leu Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro	540	545	1805
		550	
ccc tcc cgc cct ccc cca agg cct tct gtc tag agcccaaagt tcctgctctg Pro Ser Arg Pro Pro Arg Pro Ser Val	555	560	1858
ggctctctca gaaacttcag gagatgttag aacaagtctt tccagttaga gaagaggagt			1918
ggtgataaag cccactgacc ttcacacatt ctaaaaattt gttggcaatg ccagtataacc			1978
aacaatcatg atcagctgaa agaaacagat attttaaattt gccagaaaac aaatgtatgag			2038
gcaactacag tcagattt agccagccat ctatcacctc tagaaggttc cagagacagt			2098
gaaactgcaa gatgctctca acaggattt gtctcatgga gaccagtaag aaaatcattt			2158
atctgaaggt gaaatgcaga gttggataag aaatacattt ctgggtttct aaaatgctgc			2218
cttcctgcct ctactccacc tccatccctg gactttggac cttggccta ggagcctaag			2278
gaccttcacc cctgtgcacc acccaagaaa gaggaaaact ttgcctacaa ctttggaaat			2338
gctgggtcc ctgggtggt aagaaactca acatcagacg ggtatgcaga aggtgttct			2398
tctgggattt gcaggtacat aaaaaatgta tggcatctt tcctgcaaa ttcttccagt			2458
ttccaagtga gaaggggagc aggtgttac tcatggaaaa ggtatgtgc tatgttgatg			2518
tgtaagtgaa atcagttgtg tgcaatagac agggcgtat tcatggagc atcagccagt			2578
ttctaaaacc cacaggccat cagcagctag aggtggctgg cttggccag acatggaccc			2638
taaatcaaca gacaatggca ttgtcgaaga gcaacctgtt aatgaatcat gttaaaaatc			2698
aaggtttggc ttcaagttaa atcacttgag gtatgaagtt tttctgttt tccagagata			2758
aacataagtt gatctccca aaataccatc attaggacct atcacacaat atcactagtt			2818
ttttttgttt gtttgtttt tgttttttt ctggtaaag ccatgcacca cagacttctg			2878
ggcagagctg agagacaatg gtcctgacat aataaggatc tttgattaac cccataagg			2938
catgtgtgtg tatacaaata tacttcttt tggctttcg acatagaacc tcagctgtt			2998
accaagggga aatacatcag atctgcaaca cagaaatgct ctgcctgaaa tttccaccat			3058
gcctaggact cacccattt atccaggctt ttctggatct gtttaatcaa taagccctat			3118
aatcacttgc taaacactgg gtttcatcac ccagggataa aaacagagat cattgtctt			3178
gacctcctgc atcagcctat tcaaaaattt ctctctct agctttccac aaatcctaaa			3238

atccctgtcc	caagccaccc	aaattctcag	atctttctg	gaacaaggca	aatataaaa	3298
taaatataca	tttagtggct	tgggctatgg	tctccaaaga	tccttcaaaa	atacatcaag	3358
ccagcttcat	tcactcactt	tacttagaac	agagatataa	gggcctggga	tgcatttatt	3418
ttatcaatac	caattttgt	ggccatggca	gacattgcta	atcaatcaca	gcactatttc	3478
ctattaagcc	cactgatttc	ttcacaatcc	ttctcaaatt	acaattccaa	agagccgcca	3538
ctcaacagtc	agatgaaccc	aacagtcaga	tgagagaaat	gaaccctact	tgctatctct	3598
atcttagaaa	gcaaaaacaa	acaggagttt	ccagggagaa	tggaaagcc	agggggcata	3658
aaaggtacag	tcagggaaa	atagatctag	gcagagtgcc	ttagtcaggg	accacggcgc	3718
ctgaatctgc	agtgccaaca	ccaaactgac	acatctccag	gtgtacctcc	aaccctagcc	3778
ttctcccaca	gctgcctaca	acagagtctc	ccagccttct	cagagagcta	aaaccagaaa	3838
tttccagact	catgaaagca	accccccagc	ctctccccaa	ccctgcccga	ttgtctaatt	3898
tttagaacac	taggcttctt	cttcatgta	gttcctcata	agcaggggcc	agaatatctc	3958
agccacctgc	agtgacattt	ctggaccctt	gaaaaccatt	ccataggaga	atgggttccc	4018
caggctcaca	gtgtagagac	attgagccca	tcacaactgt	tttgactgct	ggcagtctaa	4078
aacagtccac	ccaccccatg	gcactgccgc	gtgattcccg	cggccattca	gaagttcaag	4138
ccgagatgct	gacgttgctg	agcaacgaga	tggtagcat	cagtgc当地	gcaccattca	4198
gcacatcagt	catatgccc	gtgcagttac	aagatgttgt	ttcggcaaag	cattttgatg	4258
gaatagggaa	ctgcaaatgt	atgatgattt	tgaaaaggct	cagcaggatt	tgttcttaaa	4318
ccgactcagt	gtgtcatccc	cggttattta	gaattacagt	taagaaggag	aaacttctat	4378
aagactgtat	gaacaaggtg	atatctcat	agtggctat	tacaggcagg	aaaatgttt	4438
aactggttta	caaaatccat	caatactgt	gtcattccct	gtaaaaggca	ggagacatgt	4498
gattatgatc	aggaaaactgc	acaaaattat	tgtttcagc	ccccgtgtta	ttgtccttt	4558
gaactgtttt	tttttttatta	aagccaaattt	tgtgttgtat	atattcgtat	tccatgtgtt	4618
agatggaagc	attccttac	cagtgtaat	aaaaagaaca	gtttagttaa	attattataa	4678
agccgatgtat	attcatggc	agtttattct	accaagctgt	gcttgggtt	tttccatgt	4738
actgtattgc	ttttataaaat	gtacaaatag	ttactgaaat	gacgagaccc	ttgtttgcac	4798
agcattaata	agaaccttga	taagaaccat	attctgttga	cagccagctc	acagtttctt	4858
gcctgaagct	tgggcaccc	tccagtgaga	cacaagatct	ctctttacc	aaagttgaga	4918
acagagctgg	tggattaatt	aatagtcttc	gatatctggc	catggtaac	ctcattgtaa	4978
ctatcatcag	aatggcaga	gatgatctt	aagtgtcaca	tacactaaag	tccaaacact	5038

atgtcagatg	ggggtaaaat	ccattaaaga	acaggaaaaa	ataattataa	gatgataagc	5098
aaatgttca	gcccaatgtc	aacccagtt	aaaaaaaaat	taatgctgtg	taaaatggtt	5158
gaattagttt	gcaaactata	taaagacata	tgcagtaaaa	agtctgttaa	tgcacatcct	5218
gtgggaatgg	agtgttctaa	ccaattgcct	tttcttgtta	tctgagctct	cctatattat	5278
catactcaga	taaccaaatt	aaaagaatta	gaatatgatt	tttaatacac	ttaacattaa	5338
actcttctaa	cttccttctt	tctgtgataa	ttcagaagat	agttatggat	cttcaatgcc	5398
tctgagtcat	tgttataaaa	aatcagttat	cactatacca	tgctatagga	gactgggcaa	5458
aacctgtaca	atgacaaccc	tggaagttgc	ttttttaaa	aaaataataa	atttcttaaa	5518
tcaaaaaaaaaa	aaaaaaaaaa	aa				5540

<210> 28
 <211> 564
 <212> PRT
 <213> human

 <400> 28

Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
 1 5 10 15

Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Arg Arg
 20 25 30

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
 35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
 50 55 60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
 130 135 140

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145 150 155 160

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
165 170 175

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
180 185 190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
195 200 205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
210 215 220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225 230 235 240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
245 250 255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
260 265 270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
275 280 285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
290 295 300

Phe Ile Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305 310 315 320

Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
325 330 335

Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
340 345 350

Glu Val Pro Pro Pro Ala Glu Glu Ser Glu Glu Asp Asp Asp
355 360 365

Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly
370 375 380

Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385 390 395 400

Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
405 410 415

Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
420 425 430

Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
435 440 445

Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
450 455 460

Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465 470 475 480

Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
485 490 495

Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
500 505 510

Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
515 520 525

Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
530 535 540

Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
545 550 555 560

Arg Pro Ser Val

<210> 29
<211> 1433
<212> DNA
<213> human

<220>
<221> CDS
<222> (148)...(900)

aac cag aac cgc ttc tgc cga ctg gag acc cag cgc cgc ctg tgc ctg	846
Asn Gln Asn Arg Phe Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu	
220 225 230	
tcc agg ccc tgc cca ccc tcc agg ggt cgc agt cca caa aac aac agt gcc	894
Ser Arg Pro Cys Pro Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala	
235 240 245	
ttc tag agccgggctg ggaatgggaa cacgggtgtcc accatccccca gctgggtggcc	950
Phe	
250	
ctgtgcctgg gcccctggct gatggaaagat ggtccgtgcc caggcccttg gctgcaggca	1010
acacttttagc ttgggtccac catgcagaac accaatatta acacgctgcc tggctctgtct	1070
ggatcccggag gtatggcaga ggtgcaagac ctagtcccct ttcctctaacc tcactgccta	1130
ggaggctggc caaggtgtcc agggtcctct agcccactcc ctgcctacac acacagccta	1190
tatcaaacat gcacacgggc gagctttctc tccgacttcc cctgggcaag agatgggaca	1250
agcagtcctt taatattttag gctgcagcag gtgctggct ggactggcca tttttctggg	1310
ggtaggatga agagaaggca cacagagatt ctggatctcc tgctgccttt tctggagttt	1370
gtaaaaattgt tcctgaatac aagcctatgc gtgaaaaaaaaaaaaaaaaaaaaaaa	1430
aaa	1433

<210> 30
 <211> 250
 <212> PRT
 <213> human

<400> 30

Met Arg Gly Thr Pro Lys Thr His Leu Leu Ala Phe Ser Leu Leu Cys	
1 5 10 15	

Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys Thr Cys	
20 25 30	

Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp	
35 40 45	

Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys	
50 55 60	

Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro	
65 70 75 80	

Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp

85

90

95

Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly Glu Thr
100 105 110

Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly Gly Phe
115 120 125

Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
130 135 140

Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys Pro Glu
145 150 155 160

Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu Pro Ala
165 170 175

Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro Gly Val
180 185 190

Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys
195 200 205

Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Arg
210 215 220

Leu Glu Thr Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Pro Pro Ser
225 230 235 240

Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe
245 250

<210> 31
<211> 2502
<212> DNA
<213> human

<220>
<221> CDS
<222> (55)..(2154)

<400> 31
gaattcgtgg gtcgtgctgc gtcgacaacg gtagtgacgc gtattgcctg gagg atg 57
Met
1

gcg gac gcc ggc att cgc cgc gtg gtt ccc agc gac ctg tat ccc ctc 105
Ala Asp Ala Gly Ile Arg Arg Val Val Pro Ser Asp Leu Tyr Pro Leu

5	10	15	
gtg ctc ggc ttc ctg cgc gat aac caa ctc tca gag gtg gcc aat aag Val Leu Gly Phe Leu Arg Asp Asn Gln Leu Ser Glu Val Ala Asn Lys 20	25	30	153
tcc gcc aaa gcg aca gga gct aca cag cag gat gcc aat gcc tct tcc Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser Ser 35	40	45	201
ctc tta gac atc tat agc ttc tgg ctc aag tct gcc aag gtc cca gag Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Ala Lys Val Pro Glu 50	55	60	249
cga aag tta cag gca aat gga cca gtg gct aag aaa gct aag aag aag Arg Lys Leu Gln Ala Asn Gly Pro Val Ala Lys Lys Ala Lys Lys Lys 70	75	80	297
gcc tca tcc agt gac agt gag gac agc agc gag gag gag gaa gtt Ala Ser Ser Ser Asp Ser Glu Asp Ser Ser Glu Glu Glu Glu Glu Val 85	90	95	345
caa ggg cct cca gca aag aag gct gct gta cct gcc aag cga gtc ggt Gln Gly Pro Pro Ala Lys Lys Ala Ala Val Pro Ala Lys Arg Val Gly 100	105	110	393
ctg cct cgg aag gct gca gcc aaa gca tca gag agt agc agc agt Leu Pro Pro Gly Lys Ala Ala Lys Ala Ser Glu Ser Ser Ser Ser 115	120	125	441
gaa gag tcc aga gat gat gat gag gag gac caa aag aaa cag cct Glu Glu Ser Arg Asp Asp Asp Glu Glu Asp Gln Lys Lys Gln Pro 130	135	140	489
gtc cag aag gga gtt aag ccc caa gca aag gca gcc aaa gct cct cct Val Gln Lys Gly Val Lys Pro Gln Ala Lys Ala Ala Lys Ala Pro Pro 150	155	160	537
aag aag gcc aag agc tct gat tct gat tct gac tca agc tcc gag gat Lys Lys Ala Lys Ser Ser Asp Ser Asp Ser Ser Ser Glu Asp 165	170	175	585
gag cca cca aag aac cag aag cca aag ata aca cct gtg aca gtt aaa Glu Pro Pro Lys Asn Gln Lys Pro Lys Ile Thr Pro Val Thr Val Lys 180	185	190	633
gct cag act aaa gcc cct ccc aaa cca gct cga gca gca cct aaa ata Ala Gln Thr Lys Ala Pro Pro Lys Pro Ala Arg Ala Ala Pro Lys Ile 195	200	205	681
gcc aat ggt aaa gca gcc agt agc agc agt agc agc agc agc agt Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser 210	215	220	729
agc agt gat gac tca gag gag aag gca gca gcc acc ccc aag aag Ser Ser Asp Asp Ser Glu Glu Lys Ala Ala Ala Thr Pro Lys Lys 230	235	240	777
act gta cct aaa aag caa gtt gtg gcc aaa gcc cca gtg aaa gca gct Thr Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Ala Ala			825

245	250	255	
acc acc cct acc cg ^g aag agt tct agc agt gag gat tcc tcc agt gac Thr Thr Pro Thr Arg Lys Ser Ser Ser Ser Glu Asp Ser Ser Ser Asp	260	265	873
	270		
gag gaa gag gag caa aaa aaa ccc atg aaa aat aaa cca ggt ccc tac Glu Glu Glu Glu Gln Lys Lys Pro Met Lys Asn Lys Pro Gly Pro Tyr	275	280	921
	285		
agt tac gcc ccc ccg cct tct gct ccc cca cca aag aag tct ctg gga Ser Tyr Ala Pro Pro Ser Ala Pro Pro Pro Lys Lys Ser Leu Gly	290	295	969
	300	305	
acc cag cct ccc aag aag gct gtg gag aag cag cag cct gtg gaa agc Thr Gln Pro Pro Lys Lys Ala Val Glu Lys Gln Gln Pro Val Glu Ser	310	315	1017
	320		
agt gaa gac agc agt gat gag tct gat tca agt tct gaa gaa gag aag Ser Glu Asp Ser Ser Asp Glu Ser Asp Ser Ser Glu Glu Glu Lys	325	330	1065
	335		
aaa ccc cca act aag gca gta gtc tct aaa gca acc act aaa cca cct Lys Pro Pro Thr Lys Ala Val Val Ser Lys Ala Thr Thr Lys Pro Pro	340	345	1113
	350		
cca gca aag aaa gca gca gag agc tct tca gac agc tca gac tct gac Pro Ala Lys Lys Ala Ala Glu Ser Ser Asp Ser Ser Asp Ser Asp	355	360	1161
	365		
agc tct gag gat gat gaa gct cct tct aag cca gct ggt acc acc aag Ser Ser Glu Asp Asp Glu Ala Pro Ser Lys Pro Ala Gly Thr Thr Lys	370	375	1209
	380	385	
aat tct tca aat aag cca gct gtc acc acc aag tca cct gca gtg aag Asn Ser Ser Asn Lys Pro Ala Val Thr Thr Lys Ser Pro Ala Val Lys	390	395	1257
	400		
cca gct gca gcc ccc aag caa cct gtg ggc ggt ggc cag aag ctt ctg Pro Ala Ala Ala Pro Lys Gln Pro Val Gly Gly Gln Lys Leu Leu	405	410	1305
	415		
acg aga aag gct gac agc agc tcc agc gag gaa gag agc agc tcc agt Thr Arg Lys Ala Asp Ser Ser Ser Glu Glu Glu Ser Ser Ser Ser	420	425	1353
	430		
gag gag gag aag aca aag aag atg gtg gcc acc act aag ccc aag gcg Glu Glu Glu Lys Thr Lys Lys Met Val Ala Thr Thr Lys Pro Lys Ala	435	440	1401
	445		
act gcc aaa gca gct cta tct ctg cct gcc aag cag gct cct cag ggt Thr Ala Lys Ala Ala Leu Ser Leu Pro Ala Lys Gln Ala Pro Gln Gly	450	455	1449
	460	465	
agt agg gac agc agc tct gat tca gac agc tcc agc agt gag gag gag Ser Arg Asp Ser Ser Asp Ser Asp Ser Ser Ser Glu Glu Glu Glu	470	475	1497
	480		
gaa gag aag aca tct aag tct gca gtt aag aag aag cca cag aag gta Glu Glu Lys Thr Ser Ala Val Lys Lys Pro Gln Lys Val			1545

485	490	495	
gca gga ggt gca gcc cct tcc aag cca gcc tct gca aag aaa gga aag Ala Gly Gly Ala Ala Pro Ser Lys Pro Ala Ser Ala Lys Lys Gly Lys 500 505 510			1593
gct gag agc agc aac agt tct tct gat gac tcc agt gag gaa gag Ala Glu Ser Ser Asn Ser Ser Ser Asp Asp Ser Ser Glu Glu Glu 515 520 525			1641
gaa gag aag ctc aag ggc aag ggc tct cca aga cca caa gcc ccc aag Glu Glu Lys Leu Lys Gly Lys Ser Pro Arg Pro Gln Ala Pro Lys 530 535 540 545			1689
gcc aat ggc acc tct gca ctg act gcc cag aat gga aaa gca gct aag Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala Lys 550 555 560			1737
aac agt gag gag gag gaa gaa aag aag gcg gca gtg gta gtt Asn Ser Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val Val 565 570 575			1785
tcc aaa tca ggt tca tta aag aag cgg aag cag aat gag gct gcc aag Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala Lys 580 585 590			1833
gag gca gag act cct cag gcc aag aag ata aag ctt cag acc cct aac Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro Asn 595 600 605			1881
aca ttt cca aaa agg aag aaa gga gaa aaa agg gca tca tcc cca ttc Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro Phe 610 615 620 625			1929
cga agg gtc agg gag gag gaa att gag gtg gat tca cga gtt gcg gac Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala Asp 630 635 640			1977
aac tcc ttt gat gcc aag cga ggt gca gcc gga gac tgg gga gag cga Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu Arg 645 650 655			2025
gcc aat cag gtt ttg aag ttc acc aaa ggc aag tcc ttt cgg cat gag Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His Glu 660 665 670			2073
aaa acc aag aag cgg ggc agc tac cgg gga ggc tca atc tct gtc Lys Thr Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile Ser Val 675 680 685			2121
cag gtc aat tct att aag ttt gac agc gag tga cctgaggcca tttcggtga Gln Val Asn Ser Ile Lys Phe Asp Ser Glu 690 695			2174
agcaagggtg atgatcgag actacttact ttctccagtg gacctggaa ccctcaggc tctaggtgag ggtcttgatg aggacagaag ttttagatgt gtcctaagac tttacagtgt			2234 2294
aacatcctct ctggccttt tctgtgttcc tagtttgta cagacttggtt tttgagtgtt			2354

gagtagcagg gacaaaataa ggaaatgtt aaaaaaataa aaattcattt tcattgttgc 2414
ctccttcctt ttctgtgaaa gtcctcatac tgagaaattt gtatattttt tattaaatca 2474
cttactattt aaaaaaaaaa aggaattc 2502

<210> 32
<211> 699
<212> PRT
<213> human

<400> 32

Met Ala Asp Ala Gly Ile Arg Arg Val Val Pro Ser Asp Leu Tyr Pro
1 5 10 15

Leu Val Leu Gly Phe Leu Arg Asp Asn Gln Leu Ser Glu Val Ala Asn
20 25 30

Lys Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser
35 40 45

Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Ala Lys Val Pro
50 55 60

Glu Arg Lys Leu Gln Ala Asn Gly Pro Val Ala Lys Lys Ala Lys Lys
65 70 75 80

Lys Ala Ser Ser Ser Asp Ser Glu Asp Ser Ser Glu Glu Glu Glu Glu
85 90 95

Val Gln Gly Pro Pro Ala Lys Lys Ala Ala Val Pro Ala Lys Arg Val
100 105 110

Gly Leu Pro Pro Gly Lys Ala Ala Lys Ala Ser Glu Ser Ser Ser
115 120 125

Ser Glu Glu Ser Arg Asp Asp Asp Asp Glu Glu Asp Gln Lys Lys Gln
130 135 140

Pro Val Gln Lys Gly Val Lys Pro Gln Ala Lys Ala Ala Lys Ala Pro
145 150 155 160

Pro Lys Lys Ala Lys Ser Ser Asp Ser Asp Ser Asp Ser Ser Ser Glu
165 170 175

Asp Glu Pro Pro Lys Asn Gln Lys Pro Lys Ile Thr Pro Val Thr Val
180 185 190

Lys Ala Gln Thr Lys Ala Pro Pro Lys Pro Ala Arg Ala Ala Pro Lys
195 200 205

Ile Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser
210 215 220

Ser Ser Ser Asp Asp Ser Glu Glu Glu Lys Ala Ala Ala Thr Pro Lys
225 230 235 240

Lys Thr Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Ala
245 250 255

Ala Thr Thr Pro Thr Arg Lys Ser Ser Ser Ser Glu Asp Ser Ser Ser
260 265 270

Asp Glu Glu Glu Glu Gln Lys Lys Pro Met Lys Asn Lys Pro Gly Pro
275 280 285

Tyr Ser Tyr Ala Pro Pro Ser Ala Pro Pro Pro Lys Lys Ser Leu
290 295 300

Gly Thr Gln Pro Pro Lys Lys Ala Val Glu Lys Gln Gln Pro Val Glu
305 310 315 320

Ser Ser Glu Asp Ser Ser Asp Glu Ser Asp Ser Ser Ser Glu Glu Glu
325 330 335

Lys Lys Pro Pro Thr Lys Ala Val Val Ser Lys Ala Thr Thr Lys Pro
340 345 350

Pro Pro Ala Lys Lys Ala Ala Glu Ser Ser Ser Asp Ser Ser Asp Ser
355 360 365

Asp Ser Ser Glu Asp Asp Glu Ala Pro Ser Lys Pro Ala Gly Thr Thr
370 375 380

Lys Asn Ser Ser Asn Lys Pro Ala Val Thr Thr Lys Ser Pro Ala Val
385 390 395 400

Lys Pro Ala Ala Ala Pro Lys Gln Pro Val Gly Gly Gly Gln Lys Leu
405 410 415

Leu Thr Arg Lys Ala Asp Ser Ser Ser Ser Glu Glu Glu Ser Ser Ser
420 425 430

Ser Glu Glu Glu Lys Thr Lys Lys Met Val Ala Thr Thr Lys Pro Lys
435 440 445

Ala Thr Ala Lys Ala Ala Leu Ser Leu Pro Ala Lys Gln Ala Pro Gln
450 455 460

Gly Ser Arg Asp Ser Ser Ser Asp Ser Asp Ser Ser Ser Glu Glu
465 470 475 480

Glu Glu Glu Lys Thr Ser Lys Ser Ala Val Lys Lys Lys Pro Gln Lys
485 490 495

Val Ala Gly Gly Ala Ala Pro Ser Lys Pro Ala Ser Ala Lys Lys Gly
500 505 510

Lys Ala Glu Ser Ser Asn Ser Ser Ser Asp Asp Ser Ser Glu Glu
515 520 525

Glu Glu Glu Lys Leu Lys Gly Lys Gly Ser Pro Arg Pro Gln Ala Pro
530 535 540

Lys Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala
545 550 555 560

Lys Asn Ser Glu Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val
565 570 575

Val Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala
580 585 590

Lys Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro
595 600 605

Asn Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro
610 615 620

Phe Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala
625 630 635 640

Asp Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu
645 650 655

Arg Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His
660 665 670

Glu Lys Thr Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile Ser
675 680 685

Val Gln Val Asn Ser Ile Lys Phe Asp Ser Glu
690 695

<210> 33
<211> 4538
<212> DNA
<213> human

<220>
<221> CDS
<222> (26)...(4012)

<400> 33
tcgtgtttcg gtgagtggtgg cggag atg gag agc cgg gat ccc gcc cag ccg 52
Met Glu Ser Arg Asp Pro Ala Gln Pro
1 5

atg tcg cct gga gaa gcg acg cag agt ggc gcc cgg cct gcc gac cgc 100
Met Ser Pro Gly Ala Thr Gln Ser Gly Ala Arg Pro Ala Asp Arg
10 15 20 25

tat ggc cta ttg aag cac agt cgc gag ttc ttg gac ttc ttc tgg gac 148
Tyr Gly Leu Leu Lys His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp
30 35 40

att gcg aag cct gag cag gag acg cga ctt gcg gcc acg gag aag ctg 196
Ile Ala Lys Pro Glu Gln Glu Thr Arg Leu Ala Ala Thr Glu Lys Leu
45 50 55

ctg gag tat ctg cgt ggc agg ccg aag ggg tcc gag atg aaa tat gcc 244
Leu Glu Tyr Leu Arg Gly Arg Pro Lys Gly Ser Glu Met Lys Tyr Ala
60 65 70

ctg aag cgt cta atc acg gga ctc ggg gtc ggg cga gaa aca gcc cgg 292
Leu Lys Arg Leu Ile Thr Gly Leu Gly Val Gly Arg Glu Thr Ala Arg
75 80 85

ccc tgc tac agt ttg gcc ctg gca cag ctg tta cag tct ttt gaa gac 340
Pro Cys Tyr Ser Leu Ala Leu Ala Gln Leu Leu Gln Ser Phe Glu Asp
90 95 100 105

ctc ccc ttg tgc agc atc ctg cag cag ata caa gaa aaa tat gac ctg 388
Leu Pro Leu Cys Ser Ile Leu Gln Gln Ile Gln Glu Lys Tyr Asp Leu
110 115 120

cat cag gtg aag aag gca atg ctg aga cct gct ctc ttt gca aac ctg 436
His Gln Val Lys Lys Ala Met Leu Arg Pro Ala Leu Phe Ala Asn Leu
125 130 135

ttt gga gtg ctc gcc ctc ttt cag tca ggt cgg ctg gtg aag gac cag 484
Phe Gly Val Leu Ala Leu Phe Gln Ser Gly Arg Leu Val Lys Asp Gln
140 145 150

gag gca ctg atg aag tcg gtg aag ctg ctg cag gcc ctg gcc cag tac Glu Ala Leu Met Lys Ser Val Lys Leu Leu Gln Ala Leu Ala Gln Tyr 155 160 165	532
caa aac cac ttg cag gag cag ccc cg ^g aag gcc ctg gtg gac atc ctc Gln Asn His Leu Gln Glu Gln Pro Arg Lys Ala Leu Val Asp Ile Leu 170 175 180 185	580
tcc gag gtc tcg aag gcc aca ttg cag gag atc ctg ccg gag gtc ctc Ser Glu Val Ser Lys Ala Thr Leu Gln Glu Ile Leu Pro Glu Val Leu 190 195 200	628
aaa gcc gac ttg aat ata ata ctc agc tcc cct gaa cag cta gag ctc Lys Ala Asp Leu Asn Ile Ile Leu Ser Ser Pro Glu Gln Leu Glu Leu 205 210 215	676
ttc ctc ctg gcc cag cag aag gtg ccc tcc aag ctc aag aag ctg gtg Phe Leu Leu Ala Gln Gln Lys Val Pro Ser Lys Leu Lys Lys Leu Val 220 225 230	724
gga tcc gtg aac cta ttc tca gat gag aat gtc ccc agg ctg gtg aat Gly Ser Val Asn Leu Phe Ser Asp Glu Asn Val Pro Arg Leu Val Asn 235 240 245	772
gtg ctg aag atg gcc gcc tcc tct gtg aag aag gac cgc aag ctg ccc Val Leu Lys Met Ala Ala Ser Ser Val Lys Lys Asp Arg Lys Leu Pro 250 255 260 265	820
gcc att gct ctg gac ctg ctc cgc ctg gcg ctc aag gaa gac aag ttc Ala Ile Ala Leu Asp Leu Leu Arg Leu Ala Leu Lys Glu Asp Lys Phe 270 275 280	868
cca cgg ttc tgg aag gag gtg gtg gaa caa ggg ctg ctg aag atg cag Pro Arg Phe Trp Lys Glu Val Val Glu Gln Gly Leu Leu Lys Met Gln 285 290 295	916
ttc tgg cca gcc agc tac ctg tgt ttc cac ctg ctg ggc gcg gcc ctg Phe Trp Pro Ala Ser Tyr Leu Cys Phe His Leu Leu Gly Ala Ala Leu 300 305 310	964
ccc ctg ctg acc aag gag cag ctg cac ctg gtg atg cag gga gac gtg Pro Leu Leu Thr Lys Glu Gln Leu His Leu Val Met Gln Gly Asp Val 315 320 325	1012
atc cgc cat tac ggg gag cac gtg tgc act gct aag ctc cca aag cag Ile Arg His Tyr Gly Glu His Val Cys Thr Ala Lys Leu Pro Lys Gln 330 335 340 345	1060
ttc aag ttt gcc cca gag atg gac gat tac gtg ggc acc ttc cta gag Phe Lys Phe Ala Pro Glu Met Asp Asp Tyr Val Gly Thr Phe Leu Glu 350 355 360	1108
ggg tgc cag gat gac cct gag cgg cag ctg gcc gtg cta gtg gcc ttc Gly Cys Gln Asp Asp Pro Glu Arg Gln Leu Ala Val Leu Val Ala Phe 365 370 375	1156
tca tct gtc acc aac caa ggc ctc cct gtc acg cct act ttc tgg cgg Ser Ser Val Thr Asn Gln Gly Leu Pro Val Thr Pro Thr Phe Trp Arg 380 385 390	1204

gtc gtg cgg ttc ctg agc cct ccg gcc ctg cag ggc tat gtg gcc tgg		1252
Val Val Arg Phe Leu Ser Pro Pro Ala Leu Gln Gly Tyr Val Ala Trp		
395 400 405		
ctg cgg gcc atg ttt ctc cag cca gac ctg gac tcc ttg gtt gac ttc		1300
Leu Arg Ala Met Phe Leu Gln Pro Asp Leu Asp Ser Leu Val Asp Phe		
410 415 420 425		
agc acc aac aac cag aag aaa gcc cag gat tca tcg ctc cac atg cct		1348
Ser Thr Asn Asn Gln Lys Lys Ala Gln Asp Ser Ser Leu His Met Pro		
430 435 440		
gag cga gct gtg ttc cgg ctg agg aaa tgg atc atc ttt cga ttg gtg		1396
Glu Arg Ala Val Phe Arg Leu Arg Lys Trp Ile Ile Phe Arg Leu Val		
445 450 455		
agc att gtg gac agc ctg cac ctg gag atg gag gag gcc ttg act gag		1444
Ser Ile Val Asp Ser Leu His Leu Glu Met Glu Glu Ala Leu Thr Glu		
460 465 470		
cag gtg gcc agg ttt tgt ttg ttc cac tcg ttc ttt gtc aca aag aag		1492
Gln Val Ala Arg Phe Cys Leu Phe His Ser Phe Phe Val Thr Lys Lys		
475 480 485		
ccc aca tcc cag atc cct gag aca aag cac ccg ttc tcc ttc cct ttg		1540
Pro Thr Ser Gln Ile Pro Glu Thr Lys His Pro Phe Ser Phe Pro Leu		
490 495 500 505		
gaa aac cag gcc cga gag gct gtc agc agt gcc ttc ttc agt ctg ttg		1588
Glu Asn Gln Ala Arg Glu Ala Val Ser Ser Ala Phe Phe Ser Leu Leu		
510 515 520		
cag acc ctc agc acg cag ttc aag cag gca ccg ggc cag acc cag ggt		1636
Gln Thr Leu Ser Thr Gln Phe Lys Gln Ala Pro Gly Gln Thr Gln Gly		
525 530 535		
ggg cag ccc tgg acc tac cac ctg gtg caa ttc gca gac ctc ctg ttg		1684
Gly Gln Pro Trp Thr Tyr His Leu Val Gln Phe Ala Asp Leu Leu Leu		
540 545 550		
aat cac agc cac aac gtg acc acc gtg aca ccc ttc act gcg cag cag		1732
Asn His Ser His Asn Val Thr Thr Val Thr Pro Phe Thr Ala Gln Gln		
555 560 565		
cac cag gcc tgg gac cgg atg ctg cag act ctg aag gag ctg gag gcc		1780
His Gln Ala Trp Asp Arg Met Leu Gln Thr Leu Lys Glu Leu Glu Ala		
570 575 580 585		
cac tcc gca gag gcc agg gct gct gcc ttc cag cac ctt ctg ctc ttc		1828
His Ser Ala Glu Ala Arg Ala Ala Phe Gln His Leu Leu Leu Phe		
590 595 600		
gtg ggc atc cac ctc ctc aag tcc cct gca gag agc tgt gac ctg ctg		1876
Val Gly Ile His Leu Leu Lys Ser Pro Ala Glu Ser Cys Asp Leu Leu		
605 610 615		
ggt gac atc cag acc tgc atc agg aaa agt ctg gga gag aag ccc cgc		1924
Gly Asp Ile Gln Thr Cys Ile Arg Lys Ser Leu Gly Glu Lys Pro Arg		
620 625 630		

cg ^g ag ^c cg ^c ac ^c a ^a g ^c ac ^c g ^a c c ^c c ^c g ^a a ^c c ^c g ^t g ^t g ^t g ^a g ^a	1972
Arg Ser Arg Thr Lys Thr Ile Asp Pro Gln Glu Pro Pro Trp Val Glu	
635 640 645	
gt ^g ct ^g gt ^g gag at ^c tt ^g ct ^g g ^c c ct ^g tt ^g g ^c c c ^a g ^c c ^a c c ^t c	2020
Val Leu Val Glu Ile Leu Ala Leu Leu Ala Gln Pro Ser His Leu	
650 655 660 665	
at ^g cg ^c ca ^g gt ^g g ^c c cg ^g ag ^c gt ^g t ^{tt} g ^g c c ^a c at ^c t ^g c t ^c c c ^a c ct ^g	2068
Met Arg Gln Val Ala Arg Ser Val Phe Gly His Ile Cys Ser His Leu	
670 675 680	
ac ^c cc ^g cg ^t g ^c c ct ^g ca ^g ct ^a at ^t ct ^g g ^a t gt ^g ct ^g a ^a c c ^c c g ^a g ^a cc	2116
Thr Pro Arg Ala Leu Gln Leu Ile Leu Asp Val Leu Asn Pro Glu Thr	
685 690 695	
ag ^t g ^a g ^g a ^a t g ^a c cg ^t gt ^g gt ^g ac ^g g ^a c g ^a t t ^c t g ^a t g ^a g	2164
Ser Glu Asp Glu Asn Asp Arg Val Val Val Thr Asp Asp Ser Asp Glu	
700 705 710	
cg ^g cg ^g ct ^g a ^a g ^g t g ^c a g ^a g ^a c a ^a g ^c g ^a g ^a g ^g t g ^a g ^a g ^a c a ^a c	2212
Arg Arg Leu Lys Gly Ala Glu Asp Lys Ser Glu Glu Gly Glu Asp Asn	
715 720 725	
ag ^a ag ^c t ^c a g ^a g ^g t g ^a a g ^a g ^a g ag ^c g ^a g g ^g g g ^a g ^a g ag ^c g ^a g g ^a g	2260
Arg Ser Ser Glu Ser Glu Glu Ser Glu Gly Glu Ser Glu Glu Ser Glu Glu	
730 735 740 745	
g ^a g ^g cg ^c g ^a c g ^g g g ^a t c ^a g g ^g c t ^t c c ^g g g ^a a c ^a g ct ^g at ^g	2308
Glu Glu Arg Asp Gly Asp Val Asp Gln Gly Phe Arg Glu Gln Leu Met	
750 755 760	
ac ^c gt ^g ct ^g ca ^g g ^g g a ^a g ^c g ct ^g g ^g t g ^a g ^a g g ^a c a ^g t g ^a g ^a a ^a c	2356
Thr Val Leu Gln Ala Gly Lys Ala Leu Gly Gly Glu Asp Ser Glu Asn	
765 770 775	
g ^a g ^g g ^a ct ^g g ^g g g ^a t g ^a g ^a g g ^c c at ^g at ^g g ^c c ct ^g g ^a c a ^g c a ^c t c ^t c	2404
Glu Glu Leu Gly Asp Glu Ala Met Met Ala Leu Asp Gln Ser Leu	
780 785 790	
g ^c c ag ^c c ^t c t ^{tt} g ^c c g ^a g c ^a g a ^a g ^c t c ^g t a ^c t c ^a g g ^c c c ^g g c ^g a g ^a c	2452
Ala Ser Leu Phe Ala Glu Gln Lys Leu Arg Ile Gln Ala Arg Arg Asp	
795 800 805	
g ^a g ^a a ^a a ^a ct ^g ca ^g a ^a g ^a g ^a g ^c t ct ^g c ^g g c ^g c g ^a c t ^t c c ^a g	2500
Glu Lys Asn Lys Leu Gln Lys Glu Lys Ala Leu Arg Arg Asp Phe Gln	
810 815 820 825	
at ^c cg ^g gt ^g ct ^g g ^a c ct ^g gt ^g g ^a g gt ^g ct ^a g ^t t g ^a c a ^a g ^c c ^c g ^a g ^a	2548
Ile Arg Val Leu Asp Leu Val Glu Val Leu Val Thr Lys Gln Pro Glu	
830 835 840	
aat g ^c c ct ^g g ^t c ct ^g g ^a g ct ^g ca ^g g ^c g ct ^g ct ^g ag ^c at ^c at ^c at ^c cg ^g	2596
Asn Ala Leu Val Leu Glu Leu Leu Glu Pro Leu Leu Ser Ile Ile Arg	
845 850 855	
cg ^c ag ^c ct ^g cg ^c ag ^c ag ^c t ^c c a ^{aa} c ^a g g ^a g ^a g ^c g ^a c c ^{tt} ct ^g c ^a c	2644
Arg Ser Leu Arg Ser Ser Ser Lys Gln Glu Gln Asp Leu Leu His	
860 865 870	

aag acg gcg cgc atc ttc acg cat cac ctg tgc cgt gcc cgg cgc tac Lys Thr Ala Arg Ile Phe Thr His His Leu Cys Arg Ala Arg Arg Tyr 875 880 885	2692
tgc cac gac ttg ggt gag cgc gca ggg gcc ctg cac gcc cag gtc gag Cys His Asp Leu Gly Glu Arg Ala Gly Ala Leu His Ala Gln Val Glu 890 895 900 905	2740
cgg ttg gtc cag cag gct ggc cgc cag ccc gac tcc ccc acc gcc ctc Arg Leu Val Gln Gln Ala Gly Arg Gln Pro Asp Ser Pro Thr Ala Leu 910 915 920	2788
tac cac ttc aac gcc tct ctc tac ctg ctc cgg gtc ttg aag ggc aac Tyr His Phe Asn Ala Ser Leu Tyr Leu Leu Arg Val Leu Lys Gly Asn 925 930 935	2836
act gct gag ggc tgc gtc cat gag aca cag gag aag cag aaa gct ggc Thr Ala Glu Gly Cys Val His Glu Thr Gln Glu Lys Gln Lys Ala Gly 940 945 950	2884
act gac ccc agc cac atg ccc acg ggc ccc cag gct gcc agc tgc ttg Thr Asp Pro Ser His Met Pro Thr Gly Pro Gln Ala Ala Ser Cys Leu 955 960 965	2932
gac ttg aac ctg gtc acc cgg gtc tac tcg aca gca ctg agc tcc ttc Asp Leu Asn Leu Val Thr Arg Val Tyr Ser Thr Ala Leu Ser Ser Phe 970 975 980 985	2980
ctg acc aag cgc aac agc ccc ctc aca gtt ccc atg ttc ctc agc ctc Leu Thr Lys Arg Asn Ser Pro Leu Thr Val Pro Met Phe Leu Ser Leu 990 995 1000	3028
tcc tcc cgg cac ccg gtc ctc tgt cag agc ctg ctc ccc atc ctg Phe Ser Arg His Pro Val Leu Cys Gln Ser Leu Leu Pro Ile Leu 1005 1010 1015	3073
gtc cag cat atc acg ggc ccg gtc cgg ccc cgt cat cag gcc tgc Val Gln His Ile Thr Gly Pro Val Arg Pro Arg His Gln Ala Cys 1020 1025 1030	3118
ctg ctg ctc cag aag acc ctg tcc atg cgg gag gtc agg tcg tgc Leu Leu Leu Gln Lys Thr Leu Ser Met Arg Glu Val Arg Ser Cys 1035 1040 1045	3163
ttt gag gac ccc gag tgg aag cag ctg atg ggc cag gtc cta gca Phe Glu Asp Pro Glu Trp Lys Gln Leu Met Gly Gln Val Leu Ala 1050 1055 1060	3208
aag gtc acc gag aac ttg cgc gtc ctg ggg gag gcg cag acc aag Lys Val Thr Glu Asn Leu Arg Val Leu Gly Glu Ala Gln Thr Lys 1065 1070 1075	3253
gcg cag cat cag cag gca ctg tcc ctg gag ctg ctc aac gtt Ala Gln His Gln Gln Ala Leu Ser Ser Leu Glu Leu Leu Asn Val 1080 1085 1090	3298
ctc ttc agg acc tgc aaa cat gag aag ctg acc ttg gac ctg acg Leu Phe Arg Thr Cys Lys His Glu Lys Leu Thr Leu Asp Leu Thr 1095 1100 1105	3343

gtg ctc ctg ggt	gtg ctg cag ggg caa	cag cag agc cta cag	cag	3388
Val Leu Leu Gly	Val Leu Gln Gly Gln	Gln Gln Ser Leu Gln	Gln	
1110	1115	1120		
ggg gca cac tcc	acc ggc tcc agc cgc	ctg cac gac ctc tac	tgg	3433
Gly Ala His Ser	Thr Gly Ser Ser Arg	Leu His Asp Leu Tyr	Trp	
1125	1130	1135		
cag gcc atg aaa	acc ctg gga gtc cag	cgccccc aag ttg gag	aag	3478
Gln Ala Met Lys	Thr Leu Gly Val Gln	Arg Pro Lys Leu Glu	Lys	
1140	1145	1150		
aag gat gcc aag	gag atc ccc agt gcc	acc cag agc ccc atc	agt	3523
Lys Asp Ala Lys	Glu Ile Pro Ser Ala	Thr Gln Ser Pro Ile	Ser	
1155	1160	1165		
aag aag cgg aag	aaa aag gga ttc ttg	ccagacg aag aag	cgc	3568
Lys Lys Arg Lys	Lys Lys Gly Phe Leu	Pro Glu Thr Lys Lys	Arg	
1170	1175	1180		
aag aaa cgc aag	tca gag gat ggc acg	ccagcg gag gat ggc	aca	3613
Lys Lys Arg Lys	Ser Glu Asp Gly Thr	Pro Ala Glu Asp Gly	Thr	
1185	1190	1195		
cct gca gcc acc	ggc ggg agc cag ccc	ccc agc atg ggc agg	aag	3658
Pro Ala Ala Thr	Gly Gly Ser Gln Pro	Pro Ser Met Gly Arg	Lys	
1200	1205	1210		
aag agg aac agg	aca aag gct aag gtc	ccagcc cag gca aac	ggg	3703
Lys Arg Asn Arg	Thr Lys Ala Lys Val	Pro Ala Gln Ala Asn	Gly	
1215	1220	1225		
acg cca acc acc	aag agt cca gcc cct	ggccccc acc cgg agc		3748
Thr Pro Thr Thr	Lys Ser Pro Ala Pro	Gly Ala Pro Thr Arg	Ser	
1230	1235	1240		
ccc agc acc cct	gcc aaa tcc cca aaa	ctg cag aag aaa aac	cag	3793
Pro Ser Thr Pro	Ala Lys Ser Pro Lys	Leu Gln Lys Lys Asn	Gln	
1245	1250	1255		
aag ccg tcc cag	gtg aat gga gct ccc	ggg tcc ccc acg gaa	cct	3838
Lys Pro Ser Gln	Val Asn Gly Ala Pro	Gly Ser Pro Thr Glu	Pro	
1260	1265	1270		
gca ggc caa aag	cag cat cag aag gct	ctt ccc aaa aag ggg	gtc	3883
Ala Gly Gln Lys	Gln His Gln Lys Ala	Leu Pro Lys Lys Gly	Val	
1275	1280	1285		
ttg ggc aaa tca	cca ctg tcc gcg ctg	gca cgg aaa aag gca	agg	3928
Leu Gly Lys Ser	Pro Leu Ser Ala Leu	Ala Arg Lys Lys Ala	Arg	
1290	1295	1300		
ctg tct ttg gtc	atc agg agt ccc agc	ctg ctt cag agt ggg	gcc	3973
Leu Ser Leu Val	Ile Arg Ser Pro Ser	Leu Leu Gln Ser Gly	Ala	
1305	1310	1315		
aag aag aaa gca	cag gtg agg aag gca	ggg aag ccc tga gcacaggtac		4022
Lys Lys Lys Ala	Gln Val Arg Lys Ala	Gly Lys Pro		
1320	1325			

ggggcccccct cagccccctgc ctccatctgc ctgagacgcc taaaaaaaaac	4082
catgattta atacgcaagc tgtttctaag gcgctgccac tggggagggt ggctgtgcc	4142
gcctgcccgg gcacccctgct ctggcaagca cagcctgagc cattcctgctg ggggtcccag	4202
ggtcagaga cctccccacc cccagttctg ggctgggatc ctggctccag ggccatgtcc	4262
agggctctgg tggttgcctg gggtggtgca tggtgatgtg ctggctgcag gcaggtgtga	4322
ccatctctcg tgcctgccac ctcttgcac ccaggcttt ttgctgtgag ggagccacca	4382
gggggtgatt taaataggtt tatttcttca tttacaagag gaatatattt ggcttctctc	4442
ttaagactct gagattcaca atcagcagct ctaaaaaata aaggagcagt ttggcttccg	4502
gaaggaagag gaggctaaaa aaaaaaaaaa aaaaaa	4538

<210> 34
 <211> 1328
 <212> PRT
 <213> human

 <400> 34

Met Glu Ser Arg Asp Pro Ala Gln Pro Met Ser Pro Gly Glu Ala Thr
 1 5 10 15

Gln Ser Gly Ala Arg Pro Ala Asp Arg Tyr Gly Leu Leu Lys His Ser
 20 25 30

Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Glu Gln Glu
 35 40 45

Thr Arg Leu Ala Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Gly Arg
 50 55 60

Pro Lys Gly Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly
 65 70 75 80

Leu Gly Val Gly Arg Glu Thr Ala Arg Pro Cys Tyr Ser Leu Ala Leu
 85 90 95

Ala Gln Leu Leu Gln Ser Phe Glu Asp Leu Pro Leu Cys Ser Ile Leu
 100 105 110

Gln Gln Ile Gln Glu Lys Tyr Asp Leu His Gln Val Lys Lys Ala Met
 115 120 125

Leu Arg Pro Ala Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe

130

135

140

Gln Ser Gly Arg Leu Val Lys Asp Gln Glu Ala Leu Met Lys Ser Val
145 150 155 160

Lys Leu Leu Gln Ala Leu Ala Gln Tyr Gln Asn His Leu Gln Glu Gln
165 170 175

Pro Arg Lys Ala Leu Val Asp Ile Leu Ser Glu Val Ser Lys Ala Thr
180 185 190

Leu Gln Glu Ile Leu Pro Glu Val Leu Lys Ala Asp Leu Asn Ile Ile
195 200 205

Leu Ser Ser Pro Glu Gln Leu Glu Leu Phe Leu Ala Gln Gln Lys
210 215 220

Val Pro Ser Lys Leu Lys Lys Leu Val Gly Ser Val Asn Leu Phe Ser
225 230 235 240

Asp Glu Asn Val Pro Arg Leu Val Asn Val Leu Lys Met Ala Ala Ser
245 250 255

Ser Val Lys Lys Asp Arg Lys Leu Pro Ala Ile Ala Leu Asp Leu Leu
260 265 270

Arg Leu Ala Leu Lys Glu Asp Lys Phe Pro Arg Phe Trp Lys Glu Val
275 280 285

Val Glu Gln Gly Leu Leu Lys Met Gln Phe Trp Pro Ala Ser Tyr Leu
290 295 300

Cys Phe His Leu Leu Gly Ala Ala Leu Pro Leu Leu Thr Lys Glu Gln
305 310 315 320

Leu His Leu Val Met Gln Gly Asp Val Ile Arg His Tyr Gly Glu His
325 330 335

Val Cys Thr Ala Lys Leu Pro Lys Gln Phe Lys Phe Ala Pro Glu Met
340 345 350

Asp Asp Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Glu
355 360 365

Arg Gln Leu Ala Val Leu Val Ala Phe Ser Ser Val Thr Asn Gln Gly

370

375

380

Leu Pro Val Thr Pro Thr Phe Trp Arg Val Val Arg Phe Leu Ser Pro
385 390 395 400

Pro Ala Leu Gln Gly Tyr Val Ala Trp Leu Arg Ala Met Phe Leu Gln
405 410 415

Pro Asp Leu Asp Ser Leu Val Asp Phe Ser Thr Asn Asn Gln Lys Lys
420 425 430

Ala Gln Asp Ser Ser Leu His Met Pro Glu Arg Ala Val Phe Arg Leu
435 440 445

Arg Lys Trp Ile Ile Phe Arg Leu Val Ser Ile Val Asp Ser Leu His
450 455 460

Leu Glu Met Glu Glu Ala Leu Thr Glu Gln Val Ala Arg Phe Cys Leu
465 470 475 480

Phe His Ser Phe Phe Val Thr Lys Lys Pro Thr Ser Gln Ile Pro Glu
485 490 495

Thr Lys His Pro Phe Ser Phe Pro Leu Glu Asn Gln Ala Arg Glu Ala
500 505 510

Val Ser Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Thr Gln Phe
515 520 525

Lys Gln Ala Pro Gly Gln Thr Gln Gly Gly Gln Pro Trp Thr Tyr His
530 535 540

Leu Val Gln Phe Ala Asp Leu Leu Leu Asn His Ser His Asn Val Thr
545 550 555 560

Thr Val Thr Pro Phe Thr Ala Gln Gln His Gln Ala Trp Asp Arg Met
565 570 575

Leu Gln Thr Leu Lys Glu Leu Glu Ala His Ser Ala Glu Ala Arg Ala
580 585 590

Ala Ala Phe Gln His Leu Leu Leu Phe Val Gly Ile His Leu Leu Lys
595 600 605

Ser Pro Ala Glu Ser Cys Asp Leu Leu Gly Asp Ile Gln Thr Cys Ile

610

615

620

Arg Lys Ser Leu Gly Glu Lys Pro Arg Arg Ser Arg Thr Lys Thr Ile
625 630 635 640

Asp Pro Gln Glu Pro Pro Trp Val Glu Val Leu Val Glu Ile Leu Leu
645 650 655

Ala Leu Leu Ala Gln Pro Ser His Leu Met Arg Gln Val Ala Arg Ser
660 665 670

Val Phe Gly His Ile Cys Ser His Leu Thr Pro Arg Ala Leu Gln Leu
675 680 685

Ile Leu Asp Val Leu Asn Pro Glu Thr Ser Glu Asp Glu Asn Asp Arg
690 695 700

Val Val Val Thr Asp Asp Ser Asp Glu Arg Arg Leu Lys Gly Ala Glu
705 710 715 720

Asp Lys Ser Glu Glu Gly Glu Asp Asn Arg Ser Ser Glu Ser Glu Glu
725 730 735

Glu Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Arg Asp Gly Asp Val
740 745 750

Asp Gln Gly Phe Arg Glu Gln Leu Met Thr Val Leu Gln Ala Gly Lys
755 760 765

Ala Leu Gly Gly Glu Asp Ser Glu Asn Glu Glu Leu Gly Asp Glu
770 775 780

Ala Met Met Ala Leu Asp Gln Ser Leu Ala Ser Leu Phe Ala Glu Gln
785 790 795 800

Lys Leu Arg Ile Gln Ala Arg Arg Asp Glu Lys Asn Lys Leu Gln Lys
805 810 815

Glu Lys Ala Leu Arg Arg Asp Phe Gln Ile Arg Val Leu Asp Leu Val
820 825 830

Glu Val Leu Val Thr Lys Gln Pro Glu Asn Ala Leu Val Leu Glu Leu
835 840 845

Leu Glu Pro Leu Leu Ser Ile Ile Arg Arg Ser Leu Arg Ser Ser Ser

850

855

860

Ser Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala Arg Ile Phe Thr
865 870 875 880

His His Leu Cys Arg Ala Arg Arg Tyr Cys His Asp Leu Gly Glu Arg
885 890 895

Ala Gly Ala Leu His Ala Gln Val Glu Arg Leu Val Gln Gln Ala Gly
900 905 910

Arg Gln Pro Asp Ser Pro Thr Ala Leu Tyr His Phe Asn Ala Ser Leu
915 920 925

Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Ala Glu Gly Cys Val His
930 935 940

Glu Thr Gln Glu Lys Gln Lys Ala Gly Thr Asp Pro Ser His Met Pro
945 950 955 960

Thr Gly Pro Gln Ala Ala Ser Cys Leu Asp Leu Asn Leu Val Thr Arg
965 970 975

Val Tyr Ser Thr Ala Leu Ser Ser Phe Leu Thr Lys Arg Asn Ser Pro
980 985 990

Leu Thr Val Pro Met Phe Leu Ser Leu Phe Ser Arg His Pro Val Leu
995 1000 1005

Cys Gln Ser Leu Leu Pro Ile Leu Val Gln His Ile Thr Gly Pro
1010 1015 1020

Val Arg Pro Arg His Gln Ala Cys Leu Leu Leu Gln Lys Thr Leu
1025 1030 1035

Ser Met Arg Glu Val Arg Ser Cys Phe Glu Asp Pro Glu Trp Lys
1040 1045 1050

Gln Leu Met Gly Gln Val Leu Ala Lys Val Thr Glu Asn Leu Arg
1055 1060 1065

Val Leu Gly Glu Ala Gln Thr Lys Ala Gln His Gln Gln Ala Leu
1070 1075 1080

Ser Ser Leu Glu Leu Leu Asn Val Leu Phe Arg Thr Cys Lys His

1085

1090

1095

Glu Lys Leu Thr Leu Asp Leu Thr Val Leu Leu Gly Val Leu Gln
1100 1105 1110

Gly Gln Gln Gln Ser Leu Gln Gln Gly Ala His Ser Thr Gly Ser
1115 1120 1125

Ser Arg Leu His Asp Leu Tyr Trp Gln Ala Met Lys Thr Leu Gly
1130 1135 1140

Val Gln Arg Pro Lys Leu Glu Lys Lys Asp Ala Lys Glu Ile Pro
1145 1150 1155

Ser Ala Thr Gln Ser Pro Ile Ser Lys Lys Arg Lys Lys Lys Gly
1160 1165 1170

Phe Leu Pro Glu Thr Lys Lys Arg Lys Lys Arg Lys Ser Glu Asp
1175 1180 1185

Gly Thr Pro Ala Glu Asp Gly Thr Pro Ala Ala Thr Gly Gly Ser
1190 1195 1200

Gln Pro Pro Ser Met Gly Arg Lys Lys Arg Asn Arg Thr Lys Ala
1205 1210 1215

Lys Val Pro Ala Gln Ala Asn Gly Thr Pro Thr Thr Lys Ser Pro
1220 1225 1230

Ala Pro Gly Ala Pro Thr Arg Ser Pro Ser Thr Pro Ala Lys Ser
1235 1240 1245

Pro Lys Leu Gln Lys Lys Asn Gln Lys Pro Ser Gln Val Asn Gly
1250 1255 1260

Ala Pro Gly Ser Pro Thr Glu Pro Ala Gly Gln Lys Gln His Gln
1265 1270 1275

Lys Ala Leu Pro Lys Lys Gly Val Leu Gly Lys Ser Pro Leu Ser
1280 1285 1290

Ala Leu Ala Arg Lys Lys Ala Arg Leu Ser Leu Val Ile Arg Ser
1295 1300 1305

Pro Ser Leu Leu Gln Ser Gly Ala Lys Lys Lys Ala Gln Val Arg
107/168

1310

1315

1320

Lys Ala Gly Lys Pro
1325

<210> 35
<211> 2427
<212> DNA
<213> human

<220>
<221> CDS
<222> (86)..(1681)

<400> 35
 gggatttgtt attgcgaatg atgtggacaa caagcgctgc tacctgctcg tccatcaagc 60
 caagaggctg agcagccccct gcata atg gtg gtc aac cat gat gcc tcc agc
 Met Val Val Asn His Asp Ala Ser Ser 112
 1 5
 ata ccc agg ctc cag ata gat gtg gac ggc agg aaa gag atc ctc ttc
 Ile Pro Arg Leu Gln Ile Asp Val Asp Gly Arg Lys Glu Ile Leu Phe 160
 10 15 20 25
 tat gat cga att tta tgt gat gtc cct tgc agt gga gac ggc act atg
 Tyr Asp Arg Ile Leu Cys Asp Val Pro Cys Ser Gly Asp Gly Thr Met 208
 30 35 40
 aga aaa aac att gat gtt tgg aaa aag tgg acc acc tta aat agc ttg
 Arg Lys Asn Ile Asp Val Trp Lys Lys Trp Thr Thr Leu Asn Ser Leu 256
 45 50 55
 cag cta cat ggc tta cag ctg cgg att gca aca cgc ggg gct gaa cag 304
 Gln Leu His Gly Leu Gln Leu Arg Ile Ala Thr Arg Gly Ala Glu Gln
 60 65 70
 ctg gct gaa ggt gga agg gtg gtg tat tcc acg tgt tca cta aac cct
 Leu Ala Glu Gly Gly Arg Val Val Tyr Ser Thr Cys Ser Leu Asn Pro 352
 75 80 85
 att gag gat gaa gca gtc ata gca tct tta ctg gaa aaa agt gaa ggt
 Ile Glu Asp Glu Ala Val Ile Ala Ser Leu Leu Glu Lys Ser Glu Gly 400
 90 95 100 105
 gct ttg gag ctt gct gat gtg tct aat gaa ctg cca ggg ctg aag tgg
 Ala Leu Glu Leu Ala Asp Val Ser Asn Glu Leu Pro Gly Leu Lys Trp 448
 110 115 120
 atg cct gga atc aca cag tgg aag gta atg acg aaa gat ggg cag tgg
 Met Pro Gly Ile Thr Gln Trp Lys Val Met Thr Lys Asp Gly Gln Trp 496
 125 130 135
 ttt aca gac tgg gac gct gtt cct cac agc aga cac acc cag atc cga
 Phe Thr Asp Trp Asp Ala Val Pro His Ser Arg His Thr Gln Ile Arg 544
 140 145 150

cct acc atg ttc cct ccg aag gac cca gaa aag ctg cag gcc atg cac Pro Thr Met Phe Pro Pro Lys Asp Pro Glu Lys Leu Gln Ala Met His 155 160 165	592
ctg gag cga tgc ctt agg ata tta ccc cat cat cag aat act gga ggg Leu Glu Arg Cys Leu Arg Ile Leu Pro His His Gln Asn Thr Gly Gly 170 175 180 185	640
ttt ttt gtg gca gta ttg gtg aaa aaa tct tca atg ccg tgg aat aaa Phe Phe Val Ala Val Leu Val Lys Lys Ser Ser Met Pro Trp Asn Lys 190 195 200	688
cgt cag cca aag ctt cag ggt aaa tct gca gag acc aga gaa agc aca Arg Gln Pro Lys Leu Gln Gly Lys Ser Ala Glu Thr Arg Glu Ser Thr 205 210 215	736
cag ctg agc cct gca gat ctc aca gaa ggg aaa ccc aca gat ccc tct Gln Leu Ser Pro Ala Asp Leu Thr Glu Gly Lys Pro Thr Asp Pro Ser 220 225 230	784
aag ctg gaa agt ccg tca ttc aca gga act ggt gac aca gaa ata gct Lys Leu Glu Ser Pro Ser Phe Thr Gly Thr Gly Asp Thr Glu Ile Ala 235 240 245	832
cat gca act gag gat tta gag aat aat ggc agt aag aaa gat ggc gtg His Ala Thr Glu Asp Leu Glu Asn Asn Gly Ser Lys Lys Asp Gly Val 250 255 260 265	880
tgt ggt cct cct cca tca aag aaa atg aag tta ttt gga ttt aaa gaa Cys Gly Pro Pro Pro Ser Lys Lys Met Lys Leu Phe Gly Phe Lys Glu 270 275 280	928
gat cca ttt gta ttt att cct gaa gat gac cca tta ttt cca cct att Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu Phe Pro Pro Ile 285 290 295	976
gag aaa ttt tat gct ttg gat cct tca ttc cca agg atg aat ttg tta Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg Met Asn Leu Leu 300 305 310	1024
act cgg act aca gaa ggg aag aaa agg cag ctc tac atg gtt tct aag Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr Met Val Ser Lys 315 320 325	1072
gag ttg cgg aat gtg ctg ctg aat aac agt gag aag atg aag gtt att Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys Met Lys Val Ile 330 335 340 345	1120
aac acg ggg atc aaa gtc tgg tgt aga aat aac agc ggt gaa gag ttt Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser Gly Glu Glu Phe 350 355 360	1168
gac tgt gct ttc cgg ctg gca cag gag gga ata tat aca ttg tat cca Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr Thr Leu Tyr Pro 365 370 375	1216
ttt att aac tca aga att att act gta tca atg gaa gat gtt aag ata Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu Asp Val Lys Ile 380 385 390	1264

ctg ttg acc cag gaa aat ccc ttt ttt aga aaa ctc agc agt gag acc Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu Ser Ser Glu Thr 395 400 405	1312
tac agt caa gca aag gac ctg gca aag gga agc atc gtg ctg aag tat Tyr Ser Gln Ala Lys Asp Leu Ala Lys Gly Ser Ile Val Leu Lys Tyr 410 415 420 425	1360
gaa cca gat tct gcg aat cca gac gct cta cag tgt ccc atc gtc tta Glu Pro Asp Ser Ala Asn Pro Asp Ala Leu Gln Cys Pro Ile Val Leu 430 435 440	1408
tgc gga tgg cgg gga aag gcc tcc att cga act ttt gtg ccc aag aat Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe Val Pro Lys Asn 445 450 455	1456
gaa cgg ctt cac tat ctc agg atg atg ggg ctg gag gta ttg gga gaa Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu Val Leu Gly Glu 460 465 470	1504
aag aag aag gaa ggg gtt atc ctc aca aat gag agt gca gcc agc acc Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Ser Ala Ala Ser Thr 475 480 485	1552
gga cag cca gac aat gac gtg act gag gga cag aga gca gga gag ccc Gly Gln Pro Asp Asn Asp Val Thr Glu Gly Gln Arg Ala Gly Glu Pro 490 495 500 505	1600
aac agc cca gat gca gaa gag gcc aac agt cca gac gtg aca gca ggc Asn Ser Pro Asp Ala Glu Glu Ala Asn Ser Pro Asp Val Thr Ala Gly 510 515 520	1648
tgt gac ccg gcg ggg gtc cat cca ccc cgg tga gcaggccaa ggcagcgggg Cys Asp Pro Ala Gly Val His Pro Pro Arg 525 530	1701
gcccacaccc ctcacacgca aaactggctt cttctggtca ctgggtctg aaaccaaatc cagagcagcc tgtggcctgt aaagcatata tttctagtga ctgcagactg gtgggatcat aggagccttc tgaatgacca ggactgctt cttggagct gatgaaaatg tactcttta gcgtgttaga aatcaactgt tttatgtt tttcttggc caagctgggt ctagtgtttc tttgctggg aatagacttt caaaagtgt acttctatca agaaacaaaa ctgcccttgc agaaatttca ggtctttgt taagcctgta ttggctttaa ggtgcagtat ttttaaatt attatttata gaaagaatct ataaattttt gggaaagtgt gttataagct ttaataatta cattgagctg cacctcagtg gtgtgtcatt aacatgcagt ggggttaata tctgaggcct cagatgactt tgtgcctttt ggaataaagg gtaaaataaa ctctccaga gtaagagctg tatcgtgaat tgtcataacta attattgagg gggacttatg tgcttttatt gaatggagtg cttacaatt tttatgttta aatggggttg ggatccttgg aatattcaa taaaattgat aaaatataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2421	1761 1821 1881 1941 2001 2061 2121 2181 2241 2301 2361

aaaaaaa

2427

<210> 36
<211> 531
<212> PRT
<213> human

<400> 36

Met Val Val Asn His Asp Ala Ser Ser Ile Pro Arg Leu Gln Ile Asp
1 5 10 15

Val Asp Gly Arg Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp
20 25 30

Val Pro Cys Ser Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp
35 40 45

Lys Lys Trp Thr Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu
50 55 60

Arg Ile Ala Thr Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Val
65 70 75 80

Val Tyr Ser Thr Cys Ser Leu Asn Pro Ile Glu Asp Glu Ala Val Ile
85 90 95

Ala Ser Leu Leu Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val
100 105 110

Ser Asn Glu Leu Pro Gly Leu Lys Trp Met Pro Gly Ile Thr Gln Trp
115 120 125

Lys Val Met Thr Lys Asp Gly Gln Trp Phe Thr Asp Trp Asp Ala Val
130 135 140

Pro His Ser Arg His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Lys
145 150 155 160

Asp Pro Glu Lys Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile
165 170 175

Leu Pro His His Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val
180 185 190

Lys Lys Ser Ser Met Pro Trp Asn Lys Arg Gln Pro Lys Leu Gln Gly
195 200 205

Lys Ser Ala Glu Thr Arg Glu Ser Thr Gln Leu Ser Pro Ala Asp Leu
210 215 220

Thr Glu Gly Lys Pro Thr Asp Pro Ser Lys Leu Glu Ser Pro Ser Phe
225 230 235 240

Thr Gly Thr Gly Asp Thr Glu Ile Ala His Ala Thr Glu Asp Leu Glu
245 250 255

Asn Asn Gly Ser Lys Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys
260 265 270

Lys Met Lys Leu Phe Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro
275 280 285

Glu Asp Asp Pro Leu Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp
290 295 300

Pro Ser Phe Pro Arg Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys
305 310 315 320

Lys Arg Gln Leu Tyr Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu
325 330 335

Asn Asn Ser Glu Lys Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp
340 345 350

Cys Arg Asn Asn Ser Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala
355 360 365

Gln Glu Gly Ile Tyr Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile
370 375 380

Thr Val Ser Met Glu Asp Val Lys Ile Leu Leu Thr Gln Glu Asn Pro
385 390 395 400

Phe Phe Arg Lys Leu Ser Ser Glu Thr Tyr Ser Gln Ala Lys Asp Leu
405 410 415

Ala Lys Gly Ser Ile Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro
420 425 430

Asp Ala Leu Gln Cys Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala
435 440 445

Ser Ile Arg Thr Phe Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg
450 455 460

Met Met Gly Leu Glu Val Leu Gly Glu Lys Lys Lys Glu Gly Val Ile
465 470 475 480

/
Leu Thr Asn Glu Ser Ala Ala Ser Thr Gly Gln Pro Asp Asn Asp Val
485 490 495

Thr Glu Gly Gln Arg Ala Gly Glu Pro Asn Ser Pro Asp Ala Glu Glu
500 505 510

Ala Asn Ser Pro Asp Val Thr Ala Gly Cys Asp Pro Ala Gly Val His
515 520 525

Pro Pro Arg
530

<210> 37
<211> 1792
<212> DNA
<213> human

<220>
<221> CDS
<222> (61)..(1281)

<400> 37
cttgaggggga agaggctgac tgtacgttcc ttctactctg gcaccactct ccaggctgcc 60

atg ggg ccc agc acc cct ctc atc ttg ttc ctt ttg tca tgg tcg 108
Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
1 5 10 15

gga ccc ctc caa gga cag cag cac cac ctt gtg gag tac atg gaa cgc 156
Gly Pro Leu Gln Gly Gln His His Leu Val Glu Tyr Met Glu Arg
20 25 30

cga cta gct gct tta gag gaa cgg ctg gcc cag tgc cag gac cag agt 204
Arg Leu Ala Ala Leu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
35 40 45

agt cgg cat gct gag ctg cgg gac ttc aag aac aag atg ctg cca 252
Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
50 55 60

ctg ctg gag gtg gca gag aag gag cgg gag gca ctc aga act gag gcc 300
Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
65 70 75 80

gac acc atc tcc ggg aga gtg gat cgt ctg gag cgg gag gta gac tat 348

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr			
85	90	95	
ctg gag acc cag aac cca gct ctg ccc tgt gta gag ttt gat gag aag			396
Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys			
100	105	110	
gtg act gga ggc cct ggg acc aaa ggc aag gga aga agg aat gag aag			444
Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys			
115	120	125	
tac gat atg gtg aca gac tgt ggc tac aca atc tct caa gtg aga tca			492
Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser			
130	135	140	
atg aag att ctg aag cga ttt ggt ggc cca gct ggt cta tgg acc aag			540
Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys			
145	150	155	160
gat cca ctg ggg caa aca gag aag atc tac gtg tta gat ggg aca cag			588
Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln			
165	170	175	
aat gac aca gcc ttt gtc ttc cca agg ctg cgt gac ttc acc ctt gcc			636
Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala			
180	185	190	
atg gct gcc cgg aaa gct tcc cga gtc cgg gtg ccc ttc ccc tgg gta			684
Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val			
195	200	205	
ggc aca ggg cag ctg gta tat ggt ggc ttt ctt tat ttt gct cgg agg			732
Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg			
210	215	220	
cct cct gga aga cct ggt gga ggt gag atg gag aac act ttg cag			780
Pro Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln			
225	230	235	240
cta atc aaa ttc cac ctg gca aac cga aca gtg gtg gac agc tca gta			828
Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val			
245	250	255	
ttc cca gca gag ggg ctg atc ccc ccc tac ggc ttg aca gca gac acc			876
Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr			
260	265	270	
tac atc gac ctg gca gct gat gag gaa ggt ctt tgg gct gtc tat gcc			924
Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala			
275	280	285	
acc cgg gag gat gac agg cac ttg tgt ctg gcc aag tta gat cca cag			972
Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln			
290	295	300	
aca ctg gac aca gag cag cag tgg gac aca cca tgt ccc aga gag aat			1020
Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn			
305	310	315	320
gct gag gct gcc ttt gtc atc tgt ggg acc ctc tat gtc gtc tat aac			1068

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn			
325	330	335	
acc cgt cct gcc agt cg ^g gcc cgc atc cag tgc tcc ttt gat gcc agc			1116
Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser			
340	345	350	
ggc acc ctg acc cct gaa cg ^g gca gca ctc cct tat ttt ccc cgc aga			1164
Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg			
355	360	365	
tat ggt gcc cat gcc agc ctc cgc tat aac ccc cga gaa cgc cag ctc			1212
Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu			
370	375	380	
tat gcc tgg gat gat ggc tac cag att gtc tat aag ctg gag atg agg			1260
Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg			
385	390	395	400
aag aaa gag gag gag gtt tga ggagctagcc ttgtttttg catctttctc			1311
Lys Lys Glu Glu Val			
405			
actccatac atttatatta tatccccact aaatttcttg ttccatcattc ttcaaatgtg			1371
ggccagttgt ggctcaaatc ctctatattt ttagccatg gcaatcaaat tctttcagct			1431
ccttgcattc atacggaact ccagatcctg agtaatcctt ttagagcccg aagagtcaaa			1491
accctcaatg ttccctcctg ctctcctgccc ccatgtcaac aaatttcagg ctaaggatgc			1551
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc agcagtgttc			1611
ttccctctag agtgacttgg ggagggagaa ataggaggag acgtccagct ctgtcctctc			1671
ttccctactc ctcccttcag tgtcctgagg aacaggactt tctccacatt gttttgtatt			1731
gcaacattt gcattaaag gaaaatccac tgctaaaaaaaaaaaaaaaaaaaaaaaaaaaa			1791
a			1792

<210> 38
 <211> 406
 <212> PRT
 <213> human

 <400> 38

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
 1 5 10 15

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 20 25 30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
 35 40 45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
65 70 75 80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
100 105 110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
115 120 125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
145 150 155 160

Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val
195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg
210 215 220

Pro Pro Gly Arg Pro Gly Gly Glu Met Glu Asn Thr Leu Gln
225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
245 250 255

Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
275 280 285

Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
340 345 350

Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg
355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg
385 390 395 400

Lys Lys Glu Glu Glu Val
405

<210> 39
<211> 1925
<212> DNA
<213> human

<220>
<221> CDS
<222> (127) .. (1278)

<400> 39
agtggagtgg gacaggtata taaaggaagt acagggcctg gggaaaggaggc cctgtctagg 60
tagctggcac caggagccgt gggcaaggga agaggccaca ccctgccttg ctctgctgca 120
gccaga atg ggt gtg aag gcg tct caa aca ggc ttt gtg gtc ctg gtg 168
Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val
1 5 10
ctg ctc cag tgc tgc tct gca tac aaa ctg gtc tgc tac tac acc agc 216
Leu Leu Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser
15 20 25 30
tgg tcc cag tac cgg gaa ggc gat ggg agc tgc ttc cca gat gcc ctt 264
Trp Ser Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu
35 40 45

gac cgc ttc ctc tgt acc cac atc atc tac agc ttt gcc aat ata agc Asp Arg Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser 50 55 60	312
aac gat cac atc gac acc tgg gag tgg aat gat gtg acg ctc tac ggc Asn Asp His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly 65 70 75	360
atg ctc aac aca ctc aag aac agg aac ccc aac ctg aag act ctc ttg Met Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu 80 85 90	408
tct gtc gga gga tgg aac ttt ggg tct caa aga ttt tcc aag ata gcc Ser Val Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala 95 100 105 110	456
tcc aac acc cag agt cgc cgg act ttc atc aag tca gta ccg cca ttc Ser Asn Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe 115 120 125	504
ctg cgc acc cat ggc ttt gat ggg ctg gac ctt gcc tgg ctc tac cct Leu Arg Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro 130 135 140	552
gga cgg aga gac aaa cag cat ttt acc acc cta atc aag gaa atg aag Gly Arg Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys 145 150 155	600
gcc gaa ttt ata aag gaa gcc cag cca ggg aaa aag cag ctc ctg ctc Ala Glu Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu 160 165 170	648
agc gca gca ctg tct gcg ggg aag gtc acc att gac agc agc tat gac Ser Ala Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp 175 180 185 190	696
att gcc aag ata tcc caa cac ctg gat ttc att agc atc atg acc tac Ile Ala Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr 195 200 205	744
gat ttt cat gga gcc tgg cgt ggg acc aca ggc cat cac agt ccc ctg Asp Phe His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu 210 215 220	792
ttc cga ggt cag gag gat gca agt cct gac aga ttc agc aac act gac Phe Arg Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp 225 230 235	840
tat gct gtg ggg tac atg ttg agg ctg ggg gct cct gcc agt aag ctg Tyr Ala Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu 240 245 250	888
gtg atg ggc atc ccc acc ttc ggg agg agc ttc act ctg gct tct tct Val Met Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser 255 260 265 270	936
gag act ggt gtt gga gcc cca atc tca gga ccg gga att cca ggc cgg Glu Thr Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg 275 280 285	984

ttc acc aag gag gca ggg acc ctt gcc tac tat gag atc tgt gac ttc	1032		
Phe Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe			
290	295	300	
ctc cgc gga gcc aca gtc cat aga acc ctc ggc cag cag gtc ccc tat	1080		
Leu Arg Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr			
305	310	315	
gcc acc aag ggc aac cag tgg gta gga tac gac gac cag gaa agc gtc	1128		
Ala Thr Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val			
320	325	330	
aaa agc aag gtg cag tac ctg aag gat agg cag ctg gca ggc gcc atg	1176		
Lys Ser Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met			
335	340	345	350
gta tgg gcc ctg gac ctg gat gac ttc cag ggc tcc ttc tgc ggc cag	1224		
Val Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln			
355	360	365	
gat ctg cgc ttc cct ctc acc aat gcc atc aag gat gca ctc gct gca	1272		
Asp Leu Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala			
370	375	380	
acg tag ccctctgttc tgcacacagc acgggggcca aggatgcccc gtcccccct	1328		
Thr			
ggctccagct ggccgggagc ctgatcacct gccctgctga gtcccaggct gagcctcagt	1388		
ctccctccct tggggcctat gcagaggc acaacacaca gattttagct cagccctgg	1448		
gggcagagag gtagggatgg ggctgtgggg atagtgaggc atcgcaatgt aagactcggg	1508		
attagtacac acttggatgat gattaatgga aatgtttaca gatccccaaag cctggcaagg	1568		
gaatttcttc aactccctgc cccctagccc tccttatcaa aggacaccat tttggcaagc	1628		
tctatcacca aggagccaaa catcctacaa gacacagtga ccatactaata tataccccct	1688		
gcaaagccag cttgaaacct tcacttagga acgtaatcgt gtcccctatc ctacttcccc	1748		
ttcctaattc cacagctgct caataaagta caagagtttta acagtgtgtt ggcgctttgc	1808		
tttggtctat ctttgagcgc ccactagacc cactggactc acctccccca tctttctgg	1868		
gttccttcct ctgagccttg ggacccctga gcttgcagag atgaaggccg ccatgtt	1925		

<210> 40
 <211> 383
 <212> PRT
 <213> human

 <400> 40

Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val Leu Leu			
1	5	10	15

Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser
20 25 30

Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu Asp Arg
35 40 45

Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Asn Asp
50 55 60

His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly Met Leu
65 70 75 80

Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser Val
85 90 95

Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala Ser Asn
100 105 110

Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe Leu Arg
115 120 125

Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Gly Arg
130 135 140

Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys Ala Glu
145 150 155 160

Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu Ser Ala
165 170 175

Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp Ile Ala
180 185 190

Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr Asp Phe
195 200 205

His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu Phe Arg
210 215 220

Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp Tyr Ala
225 230 235 240

Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu Val Met
245 250 255

Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser Glu Thr
260 265 270

Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg Phe Thr
275 280 285

Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu Arg
290 295 300

Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr Ala Thr
305 310 315 320

Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val Lys Ser
325 330 335

Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met Val Trp
340 345 350

Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln Asp Leu
355 360 365

Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala Thr
370 375 380

<210> 41
<211> 2105
<212> DNA
<213> human

<220>
<221> CDS
<222> (235)..(1752)

<400> 41
gtcccagctc gggagcacat cagaggctta gaggcgagtg ggaagggact cagacagtgc 60
aggacgagaa acgcccgcgg caccaaagcc cctcagagcg tcgccccgc ctctagttct 120
agaaaagtcaag tttcccgca ctggcacccc ggaacctcaag gggctgccga gctggggggg 180
cgctcaagct gcgaggatcc gggctgccc cgagacgagg agcgggcgcc cagg atg 237
Met
1

ggg tgc atg aag tcc aag ttc ctc cag gtc gga ggc aat aca ttc tca 285
Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe Ser
5 10 15

aaa act gaa acc agc gcc agc cca cac tgt cct gtg tac gtg ccg gat 333
Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro Asp
20 25 30

ccc aca tcc acc atc aag ccg ggg cct aat agc cac aac agc aac aca		381	
Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr			
35	40	45	
cca gga atc agg gag gca ggc tct gag gac atc atc gtg gtt gcc ctg		429	
Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu			
50	55	60	65
tat gat tac gag gcc att cac cac gaa gac ctc agc ttc cag aag ggg		477	
Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly			
70	75	80	
gac cag atg gtg gtc cta gag gaa tcc ggg gag tgg tgg aag gct cga		525	
Asp Gln Met Val Val Leu Glu Ser Gly Glu Trp Trp Lys Ala Arg			
85	90	95	
tcc ctg gcc acc cgg aag gag ggc tac atc cca agc aac tat gtc gcc		573	
Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala			
100	105	110	
cgc gtt gac tct ctg gag aca gag gag tgg ttt ttc aag ggc atc agc		621	
Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser			
115	120	125	
cgg aag gac gca gag cgc caa ctg ctg gct ccc ggc aac atg ctg ggc		669	
Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu Gly			
130	135	140	145
tcc ttc atg atc cgg gat agc gag acc act aaa gga agc tac tct ttg		717	
Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu			
150	155	160	
tcc gtg cga gac tac gac cct cgg cag gga gat acc gtc aaa cat tac		765	
Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His Tyr			
165	170	175	
aag atc cgg acc ctg gac aac ggg ggc ttc tac ata tcc ccc cga agc		813	
Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg Ser			
180	185	190	
acc ttc agc act ctg cag gag ctg gtg gac cac tac aag aag ggg aac		861	
Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly Asn			
195	200	205	
gac ggg ctc tgc cag aaa ctg tcg gtg ccc tgc atg tct tcc aag ccc		909	
Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys Pro			
210	215	220	225
cag aag cct tgg gag aaa gat gcc tgg gag atc cct cgg gaa tcc ctc		957	
Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu			
230	235	240	
aag ctg gag aag aaa ctt gga gct ggg cag ttt ggg gaa gtc tgg atg		1005	
Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met			
245	250	255	
gcc acc tac aac aag cac acc aag gtg gca gtg aag acg atg aag cca		1053	
Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro			
260	265	270	

ggg agc atg tcg gtg gag gcc ttc ctg gca gag gcc aac gtg atg aaa Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys 275 280 285	1101
act ctg cag cat gac aag ctg gtc aaa ctt cat gcg gtg gtc acc aag Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr Lys 290 295 300 305	1149
gag ccc atc tac atc atc acg gag ttc atg gcc aaa gga agc ttg ctg Glu Pro Ile Tyr Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu 310 315 320	1197
gac ttt ctg aaa agt gat gag ggc agc aag cag cca ttg cca aaa ctc Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu 325 330 335	1245
att gac ttc tca gcc cag att gca gaa ggc atg gcc ttc atc gag cag Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln 340 345 350	1293
agg aac tac atc cac cga gac ctc cga gct gcc aac atc ttg gtc tct Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser 355 360 365	1341
gca tcc ctg gtg tgt aag att gct gac ttt ggc ctg gcc cgg gtc att Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile 370 375 380 385	1389
gag gac aac gag tac acg gct cgg gaa ggg gcc aag ttc ccc atc aag Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys 390 395 400	1437
tgg aca gct cct gaa gcc atc aac ttt ggc tcc ttc acc atc aag tca Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser 405 410 415	1485
gac gtc tgg tcc ttt ggt atc ctg ctg atg gag atc gtc acc tac ggc Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly 420 425 430	1533
cgg atc cct tac cca ggg atg tca aac cct gaa gtg atc cga gct ctg Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu 435 440 445	1581
gag cgt gga tac cgg atg cct cgc cca gag aac tgc cca gag gag ctc Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu Leu 450 455 460 465	1629
tac aac atc atg atg cgc tgc tgg aaa aac cgt ccg gag gag cgg ccg Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro 470 475 480	1677
acc ttc gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc aca Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr 485 490 495	1725
gag agc cag tac caa cag cag cca tga tagggaggac cagggcaggg Glu Ser Gln Tyr Gln Gln Pro 500 505	1772

ccagggggtg cccaggtggt ggctgcaagg tggctccagc accatccgcc	1832
cccccttcct actcccagac acccaccctc gcttcagcca cagtttcctc atctgtccag	1892
tggtaggtt ggactggaaa atcttttt gactcttgca atccacaatc tgacattctc	1952
aggaagcccc caagttgata tttctatttc ctggaatggt tggattttag ttacagctgt	2012
gatttggaaag ggaaactttc aaaatagtga aatgaatatt taaataaaag atataaatgc	2072
caaagtctt accaaaaaaaaaaa aaa	2105

<210> 42
 <211> 505
 <212> PRT
 <213> human

 <400> 42

Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe	
1 5 10 15	

Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro	
20 25 30	

Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn	
35 40 45	

Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala	
50 55 60	

Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys	
65 70 75 80	

Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala	
85 90 95	

Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val	
100 105 110	

Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile	
115 120 125	

Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu	
130 135 140	

Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser	
145 150 155 160	

Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
165 170 175

Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
180 185 190

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
195 200 205

Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
210 215 220

Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
225 230 235 240

Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
245 250 255

Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
260 265 270

Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
275 280 285

Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
290 295 300

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
305 310 315 320

Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
325 330 335

Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
340 345 350

Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
355 360 365

Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
370 375 380

Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
385 390 395 400

Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
405 410 415

Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
420 425 430

Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
435 440 445

Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
450 455 460

Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
465 470 475 480

Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
485 490 495

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
500 505

<210> 43
<211> 3432
<212> DNA
<213> human

<220>
<221> CDS
<222> (248) . . (2572)

<400> 43
actccagcgc gcggctacct acgcttggtg cttgctttct ccagccatcg gagaccagag 60
ccggccccctc tgctcgagaa aggggctcag cggcgccgga agcggagggg gaccaccgtg 120
gagagcgcgg tcccagcccg gccactgcgg atccctgaaa ccaaaaagct cctgctgctt 180
ctgtaccccg cctgtccctc ccagctgcgc agggccccctt cgtggatca tcagcccgaa 240
gacaggg atg gag agg cct ctg tgc tcc cac ctc tgc agc tgc ctg gct 289
Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala
1 5 10

atg ctg gcc ctc ctg tcc ccc ctg agc ctg gca cag tat gac agc tgg 337
Met Leu Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp
15 20 25 30

ccc cat tac ccc gag tac ttc cag caa ccg gct cct gag tat cac cag 385
Pro His Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln
35 40 45

ccc cag gcc ccc gcc aac gtg gcc aag att cag ctg cgc ctg gct ggg Pro Gln Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly 50 55 60	433
cag aag agg aag cac agc gag ggc cggtg gag gtg tac tat gat ggc Gln Lys Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly 65 70 75	481
cag tgg ggc acc gtg tgc gat gac gac ttc tcc atc cac gct gcc cac Gln Trp Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His 80 85 90	529
gtc gtc tgc cgg gag ctg ggc tat gtg gag gcc aag tcc tgg act gcc Val Val Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala 95 100 105 110	577
agc tcc tcc tac ggc aag gga gaa ggg ccc atc tgg tta gac aat ctc Ser Ser Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu 115 120 125	625
cac tgt act ggc aac gag gcg acc ctt gca gca tgc acc tcc aat ggc His Cys Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly 130 135 140	673
tgg ggc gtc act gac tgc aag cac acg gag gat gtc ggt gtg gtg tgc Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys 145 150 155	721
agc gac aaa agg att cct ggg ttc aaa ttt gac aat tcg ttg atc aac Ser Asp Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn 160 165 170	769
cag ata gag aac ctg aat atc cag gtg gag gac att cgg att cga gcc Gln Ile Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala 175 180 185 190	817
atc ctc tca acc tac cgc aag cgc acc cca gtg atg gag ggc tac gtg Ile Leu Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val 195 200 205	865
gag gtg aag gag ggc aag acc tgg aag cag atc tgt gac aag cac tgg Glu Val Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp 210 215 220	913
acg gcc aag aat tcc cgc gtg gtc tgc ggc atg ttt ggc ttc cct ggg Thr Ala Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly 225 230 235	961
gag agg aca tac aat acc aaa gtg tac aaa atg ttt gcc tca cgg agg Glu Arg Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg 240 245 250	1009
aag cag cgc tac tgg cca ttc tcc atg gac tgc acc ggc aca gag gcc Lys Gln Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala 255 260 265 270	1057
cac atc tcc agc tgc aag ctg ggc ccc cag gtg tca ctg gac ccc atg His Ile Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met 275 280 285	1105

aag aat gtc acc tgc gag aat ggg ctg ccg gcc gtg gtg agt tgt gtg Lys Asn Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val 290 295 300	1153
cct ggg cag gtc ttc agc cct gac gga ccc tcg aga ttc cgg aaa gca Pro Gly Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala 305 310 315	1201
tac aag cca gag caa ccc ctg gtg cga ctg aga ggc ggt gcc tac atc Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile 320 325 330	1249
ggg gag ggc cgc gtg gag gtg ctc aaa aat gga gaa tgg ggg acc gtc Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val 335 340 345 350	1297
tgc gac gac aag tgg gac ctg gtg tcg gcc agt gtg gtc tgc aga gag Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu 355 360 365	1345
ctg ggc ttt ggg agt gcc aaa gag gca gtc act ggc tcc cga ctg ggg Leu Gly Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly 370 375 380	1393
caa ggg atc gga ccc atc cac ctc aac gag atc cag tgc aca ggc aat Gln Gly Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn 385 390 395	1441
gag aag tcc att ata gac tgc aag ttc aat gcc gag tct cag ggc tgc Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys 400 405 410	1489
aac cac gag gag gat gct ggt gtg aga tgc aac acc cct gcc atg ggc Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly 415 420 425 430	1537
ttg cag aag aag ctg cgc ctg aac ggc ggc cgc aat ccc tac gag ggc Leu Gln Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly 435 440 445	1585
cga gtg gag gtg ctg gtg gag aga aac ggg tcc ctt gtg tgg ggg atg Arg Val Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met 450 455 460	1633
gtg tgt ggc caa aac tgg ggc atc gtg gag gcc atg gtg gtc tgc cgc Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg 465 470 475	1681
cag ctg ggc ctg gga ttc gcc agc aac gcc ttc cag gag acc tgg tat Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr 480 485 490	1729
tgg cac gga gat gtc aac agc aac aaa gtg gtc atg agt gga gtg aag Trp His Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys 495 500 505 510	1777
tgc tcg gga acg gag ctg tcc ctg gcg cac tgc cgc cac gac ggg gag Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu 515 520 525	1825

gac gtg gcc tgc ccc cag ggc gga gtg cag tac ggg gcc gga gtt gcc Asp Val Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala 530 535 540	1873
tgc tca gaa acc gcc cct gac ctg gtc ctc aat gcg gag atg gtg cag Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln 545 550 555	1921
cag acc acc tac ctg gag gac cgg ccc atg ttc atg ctg cag tgt gcc Gln Thr Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala 560 565 570	1969
atg gag gag aac tgc ctc tcg gcc tca gcc gcg cag acc gac ccc acc Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr 575 580 585 590	2017
acg ggc tac cgc cgg ctc ctg cgc ttc tcc tcc cag atc cac aac aat Thr Gly Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn 595 600 605	2065
ggc cag tcc gac ttc cgg ccc aag aac ggc cgc cac gcg tgg atc tgg Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp 610 615 620	2113
cac gac tgt cac agg cac tac cac agc atg gag gtg ttc acc cac tat His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr 625 630 635	2161
gac ctg ctg aac ctc aat ggc acc aag gtg gca gag ggc cac aag gcc Asp Leu Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 640 645 650	2209
agc ttc tgc ttg gag gac aca gaa tgt gaa gga gac atc cag aag aat Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn 655 660 665 670	2257
tac gag tgt gcc aac ttc ggc gat cag ggc atc acc atg ggc tgc tgg Tyr Glu Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp 675 680 685	2305
gac atg tac cgc cat gac atc gac tgc cag tgg gtt gac atc act gac Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp 690 695 700	2353
gtg ccc cct gga gac tac ctg ttc cag gtt att aac ccc aac ttc Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe 705 710 715	2401
gag gtt gca gaa tcc gat tac tcc aac aac atc atg aaa tgc agg agc Glu Val Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser 720 725 730	2449
cgc tat gac ggc cac cgc atc tgg atg tac aac tgc cac ata ggt ggt Arg Tyr Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly 735 740 745 750	2497
tcc ttc agc gaa gag acg gaa aaa aag ttt gag cac ttc agc ggg ctc Ser Phe Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu 755 760 765	2545

tta aac aac cag ctg tcc ccg cag taa agaaggcctgc gtggtcaact	2592
Leu Asn Asn Gln Leu Ser Pro Gln	
770	
cctgtcttca ggccacacca catcttccat gggacttccc cccaaacaact gagtctgaac	2652
gaatgccacg tgccctcacc cagcccggcc cccaccctgt ccagaccctt acagctgtgt	2712
ctaaagctcag gagaaaaggg accctccat cattcatggg gggctgctac ctgacccttg	2772
gggcctgaga aggccttggg ggggtggggt ttgtccacag agctgctgga gcagcaccaa	2832
gagccagtct tgaccggat gaggcccaca gacaggttgt catcagcttgc tcccattcaa	2892
gccaccgagc tcaccacaga cacagtggag ccgcgcctt ctccagtgc acgtggacaa	2952
atgcgggctc atcagcccccc ccagagaggg tcaggccgaa ccccatattct cctcctctta	3012
ggtcattttc agcaaacttg aatatctaga cctctttcc aatgaaaccc tccagtctat	3072
tatagtcaca tagataatgg tgccacgtgt ttctgattt ggtgagctca gacttggtgc	3132
ttccctctcc acaaccccca ccccttgttt ttcaagatac tattattata tttcacaga	3192
cttttgaagc acaaatttat tggcattaa tattggacat ctggccctt ggaagtacaa	3252
atctaaggaa aaaccaaccc actgtgtaaag tgactcatct tcctgttgc ccaattctgt	3312
gggttttga ttcaacggtg ctataaccag ggtcctgggt gacagggcgc tcactgagca	3372
ccatgtgtca tcacagacac ttacacatac ttgaaacttg gaataaaaga aagattttag	3432

<210> 44
 <211> 774
 <212> PRT
 <213> human

<400> 44

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu			
1	5	10	15
10	15		

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His			
20	25	30	
30			

Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln			
35	40	45	
45			

Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys			
50	55	60	
60			

Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp			
65	70	75	80
75	80		

Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val
85 90 95

Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser
100 105 110

Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys
115 120 125

Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly
130 135 140

Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp
145 150 155 160

Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile
165 170 175

Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu
180 185 190

Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val
195 200 205

Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala
210 215 220

Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg
225 230 235 240

Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln
245 250 255

Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile
260 265 270

Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn
275 280 285

Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly
290 295 300

Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys
305 310 315 320

Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu
325 330 335

Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp
340 345 350

Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly
355 360 365

Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly
370 375 380

Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys
385 390 395 400

Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His
405 410 415

Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln
420 425 430

Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val
435 440 445

Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys
450 455 460

Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu
465 470 475 480

Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His
485 490 495

Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser
500 505 510

Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val
515 520 525

Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser
530 535 540

Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr
545 550 555 560

Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu
565 570 575

Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly
580 585 590

Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln
595 600 605

Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp
610 615 620

Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu
625 630 635 640

Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
645 650 655

Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu
660 665 670

Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met
675 680 685

Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro
690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val
705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr
725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe
740 745 750

Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu Leu Asn
755 760 765

Asn Gln Leu Ser Pro Gln
770

<210> 45
<211> 3543
<212> DNA
<213> human

<220>
<221> CDS
<222> (373) . . (3003)

<400> 45
 ccccgaaaac aggaaccctg gtggacgggt cccagcaggg ttcttcggtg cccgagaggg 60
 agcgggtgcc caagggggtg gtccctgtgg caggtcccg ggtggggcgc cggcgctccg
 ggaagagcct tccgcaggtc cccgccccgt cacgtggcgc ccggccccgg ccgctgcgg 120
 cggtccgctg gttggtcggg cgcttggtcc ggcagtttgt cggtgggcca gtggcccgtc 180
 gctcgcttct gggctctcat gtttgaaggt gggagggaca cgggagcggc cgcacacct 240
 gagccccccg gagaggagcc tcggcccccgt acccagtaag aagaggagga ggccaggcag 300
 gcaaaaggag tc atg gct tct gat gct agt cat gcg ctg gaa gct gcc ctg 360
 Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu
 1 5 10

 gag caa atg gac ggg atc att gca ggc act aaa aca ggt gca gat ctt 411
 Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu
 15 20 25

 agt gat ggt act tgt gag cct gga ctg gct tcc ccg gcc tcc tac atg 459
 Ser Asp Gly Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met
 30 35 40 45

 aac ccc ttc ccg gtg ctc cat ctc atc gag gac ttg agg ctg gcc ttg 507
 Asn Pro Phe Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu
 50 55 60

 gag atg ctg gag ctt cct cag gag aga gca gcc ctc ctg agc cag atc 555
 Glu Met Leu Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile
 65 70 75

 cct ggc cca aca gct gcc tac ata aag gaa tgg ttt gaa gag agc ttg 603
 Pro Gly Pro Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu
 80 85 90

 tcc cag gta aac cac cac agt gct gct agt aat gaa acc tac cag gaa 651
 Ser Gln Val Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu
 95 100 105

 cgc ttg gca cgt cta gaa ggg gat aag gag tcc ctc ata ttg cag gtg 747
 Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val
 110 115 120 125

 agt gtc ctc aca gac caa gta gaa gcc cag gga gaa aag att cga gac 795
 Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp
 130 135 140

 ctg gaa gtg tgt ctg gaa gga cac cag gtg aaa ctc aat gct gct gaa 843
 Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu
 145 150 155

 gag atg ctt caa cag gag ctg cta agc cgc aca tct ctt gag acc cag 891

Glu	Met	Leu	Gln	Gln	Glu	Leu	Leu	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Gln	
160						165						170				
aag	ctc	gat	ctg	atg	act	gaa	gtg	tct	gag	ctg	aag	ctc	aag	ctg	gtt	939
Lys	Leu	Asp	Leu	Met	Thr	Glu	Val	Ser	Glu	Leu	Lys	Leu	Lys	Leu	Val	
175						180					185					
ggc	atg	gag	aag	gag	cag	aga	gag	cag	gag	aag	cag	aga	aaa	gca		987
Gly	Met	Glu	Lys	Glu	Gln	Arg	Glu	Gln	Glu	Lys	Gln	Arg	Lys	Ala		
190						195					200			205		
gag	gag	tta	ctg	caa	gag	ctc	agg	cac	ctc	aaa	atc	aaa	gtg	gaa	gag	1035
Glu	Glu	Leu	Leu	Gln	Glu	Leu	Arg	His	Leu	Lys	Ile	Lys	Val	Glu	Glu	
210						215					220					
ttg	gaa	aat	gaa	agg	aat	cag	tat	gaa	tgg	aag	cta	aag	gcc	act	aag	1083
Leu	Glu	Asn	Glu	Arg	Asn	Gln	Tyr	Glu	Trp	Lys	Leu	Lys	Ala	Thr	Lys	
225						230					235					
gct	gaa	gtc	gcc	cag	ctg	caa	gaa	cag	gtg	gcc	ctg	aaa	gat	gca	gaa	1131
Ala	Glu	Val	Ala	Gln	Leu	Gln	Glu	Gln	Val	Ala	Leu	Lys	Asp	Ala	Glu	
240						245					250					
att	gag	cgt	ctg	cac	agc	cag	ctc	tcc	cg	aca	gca	gct	ctc	cac	agt	1179
Ile	Glu	Arg	Leu	His	Ser	Gln	Leu	Ser	Arg	Thr	Ala	Ala	Leu	His	Ser	
255						260					265					
gag	agt	cac	aca	gag	aga	gac	caa	gaa	att	caa	cgt	ctg	aaa	atg	ggg	1227
Glu	Ser	His	Thr	Glu	Arg	Asp	Gln	Glu	Ile	Gln	Arg	Leu	Lys	Met	Gly	
270						275					280			285		
atg	gaa	act	ttg	ctg	ctt	gcc	aat	gaa	gat	aag	gac	cgt	cg	ata	gag	1275
Met	Glu	Thr	Leu	Leu	Ala	Asn	Glu	Asp	Lys	Asp	Arg	Arg	Ile	Glu		
290						295					300					
gag	ctt	acg	ggg	ctg	tta	aac	cag	tac	cg	aag	gta	aag	gag	att	gtg	1323
Glu	Leu	Thr	Gly	Leu	Leu	Asn	Gln	Tyr	Arg	Lys	Val	Lys	Glu	Ile	Val	
305						310					315					
atg	gtc	act	caa	ggg	cct	tcg	gag	aga	act	ctc	tca	atc	aat	gaa	gaa	1371
Met	Val	Thr	Gln	Gly	Pro	Ser	Glu	Arg	Thr	Leu	Ser	Ile	Asn	Glu	Glu	
320						325					330					
gaa	ccg	gag	gga	ggt	ttc	agc	aag	tgg	aac	gct	aca	aat	aag	gac	cct	1419
Glu	Pro	Glu	Gly	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Thr	Asn	Lys	Asp	Pro	
335						340					345					
gaa	gaa	tta	ttt	aaa	caa	gag	atg	cct	cca	aga	tgt	agc	tct	cct	aca	1467
Glu	Glu	Leu	Phe	Lys	Gln	Glu	Met	Pro	Pro	Arg	Cys	Ser	Ser	Pro	Thr	
350						355					360			365		
gtg	ggg	cca	cct	cca	ttg	cca	cag	aaa	tca	ctg	gaa	acc	agg	gct	cag	1515
Val	Gly	Pro	Pro	Pro	Leu	Pro	Gln	Lys	Ser	Leu	Glu	Thr	Arg	Ala	Gln	
370						375					380					
aaa	aag	ctc	tct	tgt	agt	cta	gaa	gac	ttg	aga	agt	gaa	tct	gtg	gat	1563
Lys	Lys	Leu	Ser	Cys	Ser	Leu	Glu	Asp	Leu	Arg	Ser	Glu	Ser	Val	Asp	
385						390					395					
aag	tgt	atg	gat	ggg	aac	cag	ccc	ttc	ccg	gtg	tta	gaa	ccc	aag	gac	1611

Lys	Cys	Met	Asp	Gly	Asn	Gln	Pro	Phe	Pro	Val	Leu	Glu	Pro	Lys	Asp	
400							405				410					
agc	cct	ttc	ttg	gcg	gag	cac	aaa	tat	ccc	act	tta	cct	ggg	aag	ctt	1659
Ser	Pro	Phe	Leu	Ala	Glu	His	Lys	Tyr	Pro	Thr	Leu	Pro	Gly	Lys	Leu	
415								420				425				
tca	gga	gcc	acg	ccc	aat	gga	gag	gct	gcc	aaa	tct	cct	ccc	acc	atc	1707
Ser	Gly	Ala	Thr	Pro	Asn	Gly	Glu	Ala	Ala	Lys	Ser	Pro	Pro	Thr	Ile	
430								435			440			445		
tgc	cag	cct	gac	gcc	acg	ggg	agc	agc	ctg	ctg	agg	ctg	aga	gac	aca	1755
Cys	Gln	Pro	Asp	Ala	Thr	Gly	Ser	Ser	Leu	Leu	Arg	Leu	Arg	Asp	Thr	
450								455			460					
gaa	agt	ggc	tgg	gac	gac	act	gct	gtg	gtc	aat	gac	ctc	tca	tcc	aca	1803
Glu	Ser	Gly	Trp	Asp	Asp	Thr	Ala	Val	Val	Asn	Asp	Leu	Ser	Ser	Thr	
465							470			475						
tca	tcg	ggc	act	gaa	tca	ggt	cct	cag	tct	cct	ctg	aca	cca	gat	ggt	1851
Ser	Ser	Gly	Thr	Glu	Ser	Gly	Pro	Gln	Ser	Pro	Leu	Thr	Pro	Asp	Gly	
480							485			490						
aaa	cgg	aat	ccc	aaa	ggc	att	aag	aag	ttc	tgg	gga	aaa	atc	cga	aga	1899
Lys	Arg	Asn	Pro	Lys	Gly	Ile	Lys	Lys	Phe	Trp	Gly	Lys	Ile	Arg	Arg	
495							500			505						
act	cag	tca	gga	aat	ttc	tac	act	gac	acg	ctg	ggg	atg	gca	gag	ttt	1947
Thr	Gln	Ser	Gly	Asn	Phe	Tyr	Thr	Asp	Thr	Leu	Gly	Met	Ala	Glu	Phe	
510							515			520			525			
cga	cga	ggt	ggg	ctc	cgg	gca	acc	gca	ggg	cca	aga	ctc	tct	agg	acc	1995
Arg	Arg	Gly	Gly	Leu	Arg	Ala	Thr	Ala	Gly	Pro	Arg	Leu	Ser	Arg	Thr	
530							535			540						
agg	gac	tcc	aag	gga	cag	aaa	agt	gac	gcc	aat	gcc	ccc	ttt	gcc	cag	2043
Arg	Asp	Ser	Lys	Gly	Gln	Lys	Ser	Asp	Ala	Asn	Ala	Pro	Phe	Ala	Gln	
545							550			555						
tgg	agc	aca	gag	cgt	gtg	tgt	gca	tgg	ctg	gag	gac	ttt	ggc	ctg	gct	2091
Trp	Ser	Thr	Glu	Arg	Val	Cys	Ala	Trp	Leu	Glu	Asp	Phe	Gly	Leu	Ala	
560							565			570						
cag	tat	gtg	atc	ttt	gcc	agg	cag	tgg	gta	tct	tct	ggc	cac	acc	tta	2139
Gln	Tyr	Val	Ile	Phe	Ala	Arg	Gln	Trp	Val	Ser	Ser	Gly	His	Thr	Leu	
575							580			585						
ttg	aca	gcc	acc	cct	cag	gac	atg	gaa	aag	gag	cta	gga	att	aag	cac	2187
Leu	Thr	Ala	Thr	Pro	Gln	Asp	Met	Glu	Lys	Glu	Leu	Gly	Ile	Lys	His	
590							595			600			605			
cca	ctc	cac	agg	aag	aag	ctt	gtt	tta	gca	gtg	aaa	gcc	atc	aac	acc	2235
Pro	Leu	His	Arg	Lys	Lys	Leu	Val	Leu	Ala	Val	Lys	Ala	Ile	Asn	Thr	
610							615			620						
aaa	cag	gag	gag	aag	tct	gca	ctg	cta	gac	cac	att	tgg	gtg	aca	agg	2283
Lys	Gln	Glu	Glu	Lys	Ser	Ala	Leu	Leu	Asp	His	Ile	Trp	Val	Thr	Arg	
625							630			635						
tgg	ctt	gat	gat	att	ggc	tta	ccc	cag	tac	aaa	gac	cag	ttt	cat	gaa	2331

Trp Leu Asp Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu		
640	645	650
tct aga gtt gac aga cga atg ctg caa tac cta act gtg aac gat tta		2379
Ser Arg Val Asp Arg Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu		
655	660	665
ctc ttc tta aaa gtc acc agc caa cta cat cat ctc agc atc aaa tgt		2427
Leu Phe Leu Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys		
670	675	680
685		
gcc att cac gtg ctg cat gtc aac aag ttc aac ccc cac tgc ctg cac		2475
Ala Ile His Val Leu His Val Asn Lys Phe Asn Pro His Cys Leu His		
690	695	700
cgg cgg cca gct gat gag agt aac ctt tct cct tca gaa gtt gta cag		2523
Arg Arg Pro Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln		
705	710	715
tgg tcc aac cac agg gtg atg gag tgg tta cga tct gtg gac ctg gca		2571
Trp Ser Asn His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala		
720	725	730
gag tat gca ccc aat ctt cga ggg agt gga gtc cat gga ggc ctc att		2619
Glu Tyr Ala Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile		
735	740	745
atc ctg gag cca cgc ttc act ggg gac acc ctg gct atg ctt ctc aac		2667
Ile Leu Glu Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn		
750	755	760
765		
atc ccc cca caa aag acg ctc ctc agg cgc cac ctg acc acc aag ttc		2715
Ile Pro Pro Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe		
770	775	780
aat gcc ttg att ggt ccg gag gct gaa cag gag aag cga gag aaa atg		2763
Asn Ala Leu Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Glu Lys Met		
785	790	795
gcc tca cca gct tac aca cca ctg acc acc aca gcc aaa gtc cgg cca		2811
Ala Ser Pro Ala Tyr Thr Pro Leu Thr Thr Ala Lys Val Arg Pro		
800	805	810
agg aaa cta gga ttt tca cac ttc gga aac ata aga aaa aag aag ttc		2859
Arg Lys Leu Gly Phe Ser His Phe Gly Asn Ile Arg Lys Lys Lys Phe		
815	820	825
gat gaa tcg acg gac tac att tgc cca atg gag ccc agt gac ggt gtc		2907
Asp Glu Ser Thr Asp Tyr Ile Cys Pro Met Glu Pro Ser Asp Gly Val		
830	835	840
845		
agt gat agt cac agg gtc tac agt ggc tac cgg ggc ctc agc ccc ctt		2955
Ser Asp Ser His Arg Val Tyr Ser Gly Tyr Arg Gly Leu Ser Pro Leu		
850	855	860
gat gcc cct gaa ctg gat ggg ctg gac cag gtg gga cag att agc tga		3003
Asp Ala Pro Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser		
865	870	875
tgcccttgtc acctgccctc tgtgcaccct gagagctcac agtaacactg tgtgtgtcac		3063

catataactg cacctcaccc ccgcacgtgt gcatgactcg cagagaatat tccagcaatt 3123
gtgtacccct gggccagtct ctttgaaccc tgagggtggc caggatctgg agctgcac 3183
ctaaggggcc aggctttggg gaccattgcc aaaggtggac tcaggaggaa agacacttaa 3243
agacactttt acatgtctag taattcttga tgttcatctt cagcaccagt ggaaacacat 3303
gaacttcgat gcaggtccag agaccatgga cactcccacg aggctcagct ctcaggcacc 3363
ccctacactt cagttgaggg aaaagctcaa gtgccttagg cccgtggacc acagtcttgg 3423
ctgagatcaa agggatgagc aacagggact tctgccacag tgacaatgga attgtgttgc 3483
gccttacttc agaggtggtc tcttcttct tgtaataaaa gcaatattta tgcgaaagc 3543

<210> 46
<211> 876
<212> PRT
<213> human

<400> 46

Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu Glu Gln Met
1 5 10 15

Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu Ser Asp Gly
20 25 30

Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met Asn Pro Phe
35 40 45

Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu
50 55 60

Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile Pro Gly Pro
65 70 75 80

Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu Ser Gln Val
85 90 95

Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
130 135 140

Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu Glu Met Leu
145 150 155 160

Gln Gln Glu Leu Leu Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp
165 170 175

Leu Met Thr Glu Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu
180 185 190

Lys Glu Gln Arg Glu Gln Glu Lys Gln Arg Lys Ala Glu Glu Leu
195 200 205

Leu Gln Glu Leu Arg His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn
210 215 220

Glu Arg Asn Gln Tyr Glu Trp Lys Leu Lys Ala Thr Lys Ala Glu Val
225 230 235 240

Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu Arg
245 250 255

Leu His Ser Gln Leu Ser Arg Thr Ala Ala Leu His Ser Glu Ser His
260 265 270

Thr Glu Arg Asp Gln Glu Ile Gln Arg Leu Lys Met Gly Met Glu Thr
275 280 285

Leu Leu Leu Ala Asn Glu Asp Lys Asp Arg Arg Ile Glu Glu Leu Thr
290 295 300

Gly Leu Leu Asn Gln Tyr Arg Lys Val Lys Glu Ile Val Met Val Thr
305 310 315 320

Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile Asn Glu Glu Glu Pro Glu
325 330 335

Gly Gly Phe Ser Lys Trp Asn Ala Thr Asn Lys Asp Pro Glu Glu Leu
340 345 350

Phe Lys Gln Glu Met Pro Pro Arg Cys Ser Ser Pro Thr Val Gly Pro
355 360 365

Pro Pro Leu Pro Gln Lys Ser Leu Glu Thr Arg Ala Gln Lys Lys Leu
370 375 380

Ser Cys Ser Leu Glu Asp Leu Arg Ser Glu Ser Val Asp Lys Cys Met
385 390 395 400

Asp Gly Asn Gln Pro Phe Pro Val Leu Glu Pro Lys Asp Ser Pro Phe
405 410 415

Leu Ala Glu His Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala
420 425 430

Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ile Cys Gln Pro
435 440 445

Asp Ala Thr Gly Ser Ser Leu Leu Arg Leu Arg Asp Thr Glu Ser Gly
450 455 460

Trp Asp Asp Thr Ala Val Val Asn Asp Leu Ser Ser Thr Ser Ser Gly
465 470 475 480

Thr Glu Ser Gly Pro Gln Ser Pro Leu Thr Pro Asp Gly Lys Arg Asn
485 490 495

Pro Lys Gly Ile Lys Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser
500 505 510

Gly Asn Phe Tyr Thr Asp Thr Leu Gly Met Ala Glu Phe Arg Arg Gly
515 520 525

Gly Leu Arg Ala Thr Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Ser
530 535 540

Lys Gly Gln Lys Ser Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr
545 550 555 560

Glu Arg Val Cys Ala Trp Leu Glu Asp Phe Gly Leu Ala Gln Tyr Val
565 570 575

Ile Phe Ala Arg Gln Trp Val Ser Ser Gly His Thr Leu Leu Thr Ala
580 585 590

Thr Pro Gln Asp Met Glu Lys Glu Leu Gly Ile Lys His Pro Leu His
595 600 605

Arg Lys Lys Leu Val Leu Ala Val Lys Ala Ile Asn Thr Lys Gln Glu
610 615 620

Glu Lys Ser Ala Leu Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp
625 630 635 640

Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val
645 650 655

Asp Arg Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu
660 665 670

Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys Ala Ile His
675 680 685

Val Leu His Val Asn Lys Phe Asn Pro His Cys Leu His Arg Arg Pro
690 695 700

Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn
705 710 715 720

His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala
725 730 735

Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu
740 745 750

Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro
755 760 765

Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu
770 775 780

Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Glu Lys Met Ala Ser Pro
785 790 795 800

Ala Tyr Thr Pro Leu Thr Thr Ala Lys Val Arg Pro Arg Lys Leu
805 810 815

Gly Phe Ser His Phe Gly Asn Ile Arg Lys Lys Phe Asp Glu Ser
820 825 830

Thr Asp Tyr Ile Cys Pro Met Glu Pro Ser Asp Gly Val Ser Asp Ser
835 840 845

His Arg Val Tyr Ser Gly Tyr Arg Gly Leu Ser Pro Leu Asp Ala Pro
850 855 860

Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser
865 870 875

<210> 47
<211> 2819
<212> DNA
<213> human

<220>
<221> CDS
<222> (77)..(1180)

<400> 47
ctggggccag ctcccccag aggtggtcgg atccctctggg ctgctcggtc gatgcctgtg 60
ccactgacgt ccaggc atg agg tgg ttc ctg ccc tgg acg ctg gca gca gtg 112
Met Arg Trp Phe Leu Pro Trp Thr Leu Ala Ala Val
1 5 10
aca gca gca gcc gcc agc acc gtc ctg gcc acg gcc ctc tct cca gcc 160
Thr Ala Ala Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala
15 20 25
cct acg acc atg gac ttt acc cca gct cca ctg gag gac acc tcc tca 208
Pro Thr Thr Met Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser
30 35 40
cgc ccc caa ttc tgc aag tgg cca tgt gag tgc ccg cca tcc cca ccc 256
Arg Pro Gln Phe Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro
45 50 55 60
cgc tgc ccg ctg ggg gtc agc ctc atc aca gat ggc tgt gag tgc tgt 304
Arg Cys Pro Leu Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys
65 70 75
aag atg tgc gct cag cag ctt ggg gac aac tgc acg gag gct gcc atc 352
Lys Met Cys Ala Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile
80 85 90
tgt gac ccc cac cgg ggc ctc tac tgt gac tac agc ggg gac cgc ccg 400
Cys Asp Pro His Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro
95 100 105
agg tac gca ata gga gtg tgt gca cag gtg gtc ggt gtg ggc tgc gtc 448
Arg Tyr Ala Ile Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val
110 115 120
ctg gat ggg gtg cgc tac aac aac ggc cag tcc ttc cag cct aac tgc 496
Leu Asp Gly Val Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys
125 130 135 140
aag tac aac tgc acg tgc atc gac ggc gcg gtg ggc tgc aca cca ctg 544
Lys Tyr Asn Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu
145 150 155
tgc ctc cga gtg cgc ccc ccg cgt ctc tgg tgc ccc cac ccg cgg cgc 592
Cys Leu Arg Val Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg

160	165	170														
gtg	agc	ata	cct	ggc	cac	tgc	tgt	gag	cag	tgg	gta	tgt	gag	gac	gac	640
Val	Ser	Ile	Pro	Gly	His	Cys	Cys	Glu	Gln	Trp	Val	Cys	Glu	Asp	Asp	
175						180					185					
gcc	aag	agg	cca	cgc	aag	acc	gca	ccc	cgt	gac	aca	gga	gcc	ttc	gat	688
Ala	Lys	Arg	Pro	Arg	Lys	Thr	Ala	Pro	Arg	Asp	Thr	Gly	Ala	Phe	Asp	
190						195					200					
gct	gtg	ggt	gag	gtg	gag	gca	tgg	cac	agg	aac	tgc	ata	gcc	tac	aca	736
Ala	Val	Gly	Glu	Val	Glu	Ala	Trp	His	Arg	Asn	Cys	Ile	Ala	Tyr	Thr	
205						210					215			220		
agc	ccc	tgg	agc	cct	tgc	tcc	acc	agc	tgc	ggc	ctg	ggg	gtc	tcc	act	784
Ser	Pro	Trp	Ser	Pro	Cys	Ser	Thr	Ser	Cys	Gly	Leu	Gly	Val	Ser	Thr	
225						230					235					
cgg	atc	tcc	aat	gtt	aac	gcc	cag	tgc	tgg	cct	gag	caa	gag	agc	cgc	832
Arg	Ile	Ser	Asn	Val	Asn	Ala	Gln	Cys	Trp	Pro	Glu	Gln	Glu	Ser	Arg	
240						245					250					
ctc	tgc	aac	ttg	cgg	cca	tgc	gat	gtg	gac	atc	cat	aca	ctc	att	aag	880
Leu	Cys	Asn	Leu	Arg	Pro	Cys	Asp	Val	Asp	Ile	His	Thr	Leu	Ile	Lys	
255						260					265					
gca	ggg	aag	aag	tgt	ctg	gtg	tac	cag	cca	gag	gca	tcc	atg	aac	928	
Ala	Gly	Lys	Lys	Cys	Leu	Ala	Val	Tyr	Gln	Pro	Glu	Ala	Ser	Met	Asn	
270						275					280					
ttc	aca	ctt	gcg	ggc	tgc	atc	agc	aca	cgc	tcc	tat	caa	ccc	aag	tac	976
Phe	Thr	Leu	Ala	Gly	Cys	Ile	Ser	Thr	Arg	Ser	Tyr	Gln	Pro	Lys	Tyr	
285						290					295			300		
tgt	gga	gtt	tgc	atg	gac	aat	agg	tgc	atc	ccc	tac	aag	tct	aag	1024	
Cys	Gly	Val	Cys	Met	Asp	Asn	Arg	Cys	Cys	Ile	Pro	Tyr	Lys	Ser	Lys	
305						310					315					
act	atc	gac	gtg	tcc	ttc	cag	tgt	cct	gat	ggg	ctt	ggc	ttc	tcc	cgc	1072
Thr	Ile	Asp	Val	Ser	Phe	Gln	Cys	Pro	Asp	Gly	Leu	Gly	Phe	Ser	Arg	
320						325					330					
cag	gtc	cta	tgg	att	aat	gcc	tgc	ttc	tgt	aac	ctg	agc	tgt	agg	aat	1120
Gln	Val	Leu	Trp	Ile	Asn	Ala	Cys	Phe	Cys	Asn	Leu	Ser	Cys	Arg	Asn	
335						340					345					
ccc	aat	gac	atc	ttt	gct	gac	ttg	gaa	tcc	tac	cct	gac	ttc	tca	gaa	1168
Pro	Asn	Asp	Ile	Phe	Ala	Asp	Leu	Glu	Ser	Tyr	Pro	Asp	Phe	Ser	Glu	
350						355					360					
att	gcc	aac	tag	gcaggcacaa	atcttgggtc	ttggggacta	acccaaatgcc									1220
Ile	Ala	Asn														
365																
tgtgaaggcag	tcagccctta	tggccaataa	cttttcacca	atgagcctta	gttaccctga											1280
tctggaccct	tggcctccat	ttctgtctct	aaccattcaa	atgacgcctg	atggtgctgc											1340
tcaggcccatt	gctatgagtt	ttctccttga	tatcattcag	catctactct	aaagaaaaat											1400

gcctgtctct	agctgttctg	gactacaccc	aagcctgatc	cagccttcc	aagtcactag	1460
aagtccctgct	ggatcttgcc	taaatccaa	gaaatggaat	caggtagact	tttaatata	1520
ctaatttctt	cttagatgc	caaaccacaa	gactcttgg	gtccattcag	atgaatagat	1580
ggaatttgg	acaatagaat	aatctattat	ttggagcctg	ccaagaggta	ctgtaatggg	1640
taattctgac	gtcagcgcac	caaaactatc	ctgattccaa	atatgtatgc	acctcaagg	1700
catcaaacat	ttgccaagtg	agttgaatag	ttgcttaatt	ttgattttta	atggaaagtt	1760
gtatccatta	acctgggcat	tgtttagg	aagtttctct	tcaccctac	actgtgaagg	1820
gtacagatta	ggtttgc	agtcagaaat	aaaattt	aaacattcct	gttgatggg	1880
aaagccccca	gttaatactc	cagagacagg	gaaaggtcag	cccg	aaggaccaat	1940
tgactctcac	actgaatcag	ctgctgactg	gcagg	ggcagttgg	ccaggctt	2000
ccttgaatct	tctcccttgt	cctgcttgg	gttc	catagga	attggtaagg	2060
ggcctgtctg	ccccctgaga	gtgg	tgccct	ggaacactcc	tctactctt	2120
agagacccag	ctgcagacca	tgcc	agacccc	actgaaatga	ccaagacagg	2180
ggtgtgggtc	aaaccaagaa	gtgg	gtggccc	ttggtagcag	cctgggtga	2240
tggaggctgt	gggactccag	ggg	ccccgt	gttcaggaca	catctattgc	2300
ttcacagcct	ttcg	ttctgc	tgac	caaatg	gccagttt	2360
accggttgtt	tagaa	acaga	aatagactt	ataaagg	aaagctgaag	2420
taaaaaggaaa	agg	ttgtt	taat	gaat	cagg	2480
taatatttac	tgtt	agaatt	cttt	tattt	ggcctt	2540
gtgcttgca	tgtt	attagct	cact	gaatct	tcac	2600
atttctgttc	ttaca	aaatgt	gaa	acg	gaa	2660
cacccagttg	gtg	actgg	aag	ttg	atc	2720
catatttcc	ccct	gtttt	agag	ctt	ccaa	2780
aatggcttga	ttttt	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	2819

<210> 48
 <211> 367
 <212> PRT
 <213> human

 <400> 48

Met	Arg	Trp	Phe	Leu	Pro	Trp	Thr	Leu	Ala	Ala	Val	Thr	Ala	Ala	Ala
1								5				10			15

Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala Pro Thr Thr Met
20 25 30

Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser Arg Pro Gln Phe
35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro Arg Cys Pro Leu
50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Met Cys Ala
65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
115 120 125

Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys Lys Tyr Asn Cys
130 135 140

Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu Cys Leu Arg Val
145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg Val Ser Ile Pro
165 170 175

Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp Ala Lys Arg Pro
180 185 190

Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp Ala Val Gly Glu
195 200 205

Val Glu Ala Trp His Arg Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
210 215 220

Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr Arg Ile Ser Asn
225 230 235 240

Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
245 250 255

Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys Ala Gly Lys Lys
260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn Phe Thr Leu Ala
275 280 285

Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr Cys Gly Val Cys
290 295 300

Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Asp Val
305 310 315 320

Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg Gln Val Leu Trp
325 330 335

Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
340 345 350

Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu Ile Ala Asn
355 360 365

<210> 49
<211> 1768
<212> DNA
<213> human

<220>
<221> CDS
<222> (356) .. (868)

<400> 49
ggcacgaggc tgctgtctgc ggagggaaact gcatcgacgg acggccgccc agctacggga 60
ggacctggag tggcaactggg cgcccgacgg accatccccg ggaccgcct gcccctcggc 120
gccccgcccc gccgggcccgc tccccgtcgg gttccccagc cacagcctta cctacgggct 180
cctgactccg caaggcttcc agaagatgct cgaaccacccg gccggggcct cggggcagca 240
gtgagggagg cgtccagccc cccactcagc tcttctcctc ctgtgccagg ggctccccgg 300
gggatgagca tggtggtttt ccctcgaggc cccctggctc gggacgtctg agaag atg
Met 1

ccg gtc atg agg ctg ttc cct tgc ttc ctg cag ctc ctg gcc ggg ctg 406
Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly Leu
5 10 15

gcg ctg cct gct gtg ccc ccc cag cag tgg gcc ttg tct gct ggg aac 454
Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly Asn
20 25 30

ggc tcg tca gag gtg gaa gtg gta ccc ttc cag gaa gtg tgg ggc cgc	502
Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly Arg	
35 40 45	
agc tac tgc cgg gcg ctg gag agg ctg gtg gac gtc gtg tcc gag tac	550
Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu Tyr	
50 55 60 65	
ccc agc gag gtg gag cac atg ttc agc cca tcc tgt gtc tcc ctg ctg	598
Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu Leu	
70 75 80	
cgc tgc acc ggc tgc tgc ggc gat gag aat ctg cac tgt gtg cgc gtg	646
Arg Cys Thr Gly Cys Gly Asp Glu Asn Leu His Cys Val Pro Val	
85 90 95	
gag acg gcc aat gtc acc atg cag ctc cta aag atc cgt tct ggg gac	694
Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly Asp	
100 105 110	
cgg ccc tcc tac gtg gag ctg acg ttc tct cag cac gtt cgc tgc gaa	742
Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys Glu	
115 120 125	
tgc cgg cct ctg cgg gag aag atg aag ccg gaa agg agg aga ccc aag	790
Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro Lys	
130 135 140 145	
ggc agg ggg aag agg aga gag aag cag aga ccc aca gac tgc cac	838
Gly Arg Gly Lys Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys His	
150 155 160	
ctg tgc ggc gat gct gtt ccc cgg agg taa cccacccctt ggaggagaga	888
Leu Cys Gly Asp Ala Val Pro Arg Arg	
165 170	
gaccggcac ccggctcgta tatttattac cgtcacactc ttcagtgact cctgctggta	948
cctgcctctt atttattagc caactgtttc cctgctgaat gcctcgctcc cttcaagacg	1008
aggggcaggg aaggacagga ccctcagggaa ttcaactgcct tcaacaacgt gagagaaaga	1068
gagaagccag ccacagaccc ctgggagtt ccgcgtttgaa agaagcaaga cacgtggcct	1128
cgtgaggggc aagctaggcc ccagaggccc tggaggtctc cagggccctg cagaaggaaa	1188
gaagggggcc ctgctacctg ttcttggcc tcaggctctg cacagtcaag cagcccttgc	1248
tttcggagct cctgtccaaa agtagggatg cggatcctgc tggggccgcc acggcctggc	1308
tggtagggaaag gccggcagcg ggcggagggg atccagccac ttcccccctt tcttctgaag	1368
atcagaacat tcagctctgg agaacagtgg ttgcctgggg gctttgcca ctccttgc	1428
cccgatctt cccctcacac tttgccattt gcttgtactg ggacattgtt cttccggcc	1488
aagggtgccac caccctgccc cccctaagag acacatacag agtggggccc gggctggaga	1548
aagagctgcc tggatgagaa acagctcagc cagtgggat gaggtcacca gggaggagc	1608

ctgtgcgtcc cagctgaagg cagtggcagg ggagcagggtt ccccaagggc cctggcaccc 1668
ccacaagctg tccctgcagg gccatctgac tgccaagcca gattctcttg aataaaagtat 1728
tctagtgtgg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1768

<210> 50
<211> 170
<212> PRT
<213> human

<400> 50

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
130 135 140

Lys Gly Arg Gly Lys Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
145 150 155 160

His Leu Cys Gly Asp Ala Val Pro Arg Arg
165 170

<210> 51

<211> 3874
 <212> DNA
 <213> human

 <220>
 <221> CDS
 <222> (1)..(1902)

 <400> 51

atg	gct	cac	cta	aag	cga	cta	gta	aaa	tta	cac	att	aaa	aga	cat	tac	48
Met	Ala	His	Leu	Lys	Arg	Leu	Val	Lys	Leu	His	Ile	Lys	Arg	His	Tyr	
1			5						10				15			

cat	aaa	aag	ttc	tgg	aag	ctt	ggt	gca	gta	att	ttt	ttc	ttt	ata	ata	96
His	Lys	Lys	Phe	Trp	Lys	Leu	Gly	Ala	Val	Ile	Phe	Phe	Ile	Ile		
			20						25				30			

gtt	ttg	gtt	tta	atg	caa	aga	gaa	gta	agt	gtt	caa	tat	tcc	aaa	gag	144
Val	Leu	Val	Leu	Met	Gln	Arg	Glu	Val	Ser	Val	Gln	Tyr	Ser	Lys	Glu	
				35				40				45				

gaa	tca	agg	atg	gaa	agg	aac	atg	aaa	aac	aaa	aac	aag	atg	ttg	gat	192
Glu	Ser	Arg	Met	Glu	Arg	Asn	Met	Lys	Asn	Lys	Asn	Lys	Met	Leu	Asp	
				50				55				60				

tta	atg	cta	gaa	gct	gta	aac	aat	att	aag	gat	gcc	atg	cca	aaa	atg	240
Leu	Met	Leu	Glu	Ala	Val	Asn	Asn	Ile	Lys	Asp	Ala	Met	Pro	Lys	Met	
				65				70			75			80		

caa	ata	gga	gca	cct	gtc	agg	caa	aac	att	gat	gct	ggt	gag	aga	cct	288
Gln	Ile	Gly	Ala	Pro	Val	Arg	Gln	Asn	Ile	Asp	Ala	Gly	Glu	Arg	Pro	
				85				90				95				

tgt	ttg	caa	gga	tat	tat	aca	gca	gca	gaa	ttg	aag	cct	gtc	ctt	gac	336
Cys	Leu	Gln	Gly	Tyr	Tyr	Thr	Ala	Ala	Glu	Leu	Lys	Pro	Val	Leu	Asp	
				100				105				110				

cgt	cca	cct	cag	gat	tca	aat	gca	cct	ggt	gct	tct	ggt	aaa	gca	ttc	384
Arg	Pro	Pro	Gln	Asp	Ser	Asn	Ala	Pro	Gly	Ala	Ser	Gly	Lys	Ala	Phe	
				115				120				125				

aag	aca	acc	aat	tta	agt	gtt	gaa	gag	caa	aag	gaa	aag	gaa	cgt	ggg	432
Lys	Thr	Thr	Asn	Leu	Ser	Val	Glu	Glu	Gln	Lys	Glu	Lys	Glu	Arg	Gly	
				130				135				140				

gaa	gct	aaa	cac	tgc	ttt	aat	gct	ttc	gca	agt	gac	agg	att	tct	ttg	480
Glu	Ala	Lys	His	Cys	Phe	Asn	Ala	Phe	Ala	Ser	Asp	Arg	Ile	Ser	Leu	
				145				150			155			160		

cac	cga	gat	ctt	gga	cca	gac	act	cga	cct	cct	gaa	tgt	att	gaa	caa	528
His	Arg	Asp	Leu	Gly	Pro	Asp	Thr	Arg	Pro	Pro	Glu	Cys	Ile	Glu	Gln	
				165				170				175				

aaa	ttt	aag	cgc	tgc	cct	ccc	ctg	ccc	acc	acc	agt	gtc	ata	ata	gtt	576
Lys	Phe	Lys	Arg	Cys	Pro	Pro	Leu	Pro	Thr	Thr	Ser	Val	Ile	Ile	Val	
				180				185				190				

ttt	cat	aat	gaa	gcg	tgg	tcc	acg	ttg	ctt	aga	act	gtc	cac	agt	gtg	624
Phe	His	Asn	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	Val	His	Ser	Val	

195	200	205	
ctc tat tct tca cct gca ata ctg ctg aag gaa atc att ttg gtg gat Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp 210	215	220	672
gat gct agt gta gat gag tac tta cat gat aaa cta gat gaa tat gta Asp Ala Ser Val Asp Glu Tyr Leu His Asp Lys Leu Asp Glu Tyr Val 225	230	235	720
aaa caa ttt tct ata gta aaa ata gtc aga caa aga gaa aga aaa ggt Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Arg Glu Arg Lys Gly 245	250	255	768
ctg atc act gct cgg ttg cta gga gca aca gtc gca aca gct gaa acg Leu Ile Thr Ala Arg Leu Leu Gly Ala Thr Val Ala Thr Ala Glu Thr 260	265	270	816
ctc aca ttt tta gat gct cac tgt gag tgt ttc tat ggt tgg cta gaa Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu 275	280	285	864
cct ctg ttg gcc aga ata gct gag aac tac acg gct gtc gta agt cca Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro 290	295	300	912
gat att gca tcc ata gat ctg aac acg ttt gaa ttc aac aaa cct tct Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser 305	310	315	960
cct tat gga agt aac cat aac cgt gga aat ttt gac tgg agt ctt tca Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser 325	330	335	1008
ttt ggc tgg gag tcg ctt cct gat cat gag aag caa aga agg aaa gat Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp 340	345	350	1056
gaa acc tac cca att aaa aca ccc act ttt gca gga gga ctt ttt tcc Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser 355	360	365	1104
ata tca aaa gaa tat ttt gag tat att gga agc tat gat gaa gaa atg Ile Ser Lys Glu Tyr Phe Glu Tyr Ile Gly Ser Tyr Asp Glu Glu Met 370	375	380	1152
gaa atc tgg gga ggt gaa aat ata gaa atg tct ttc aga gta tgg caa Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln 385	390	395	1200
tgt ggt ggg cag ttg gag att atg cct tgc tct gtt gtt gga cat gtt Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val 405	410	415	1248
ttt cgc agc aaa agc cct cat agc ttt cca aaa ggc act cag gtg att Phe Arg Ser Lys Ser Pro His Ser Phe Pro Lys Gly Thr Gln Val Ile 420	425	430	1296
gct aga aac caa gtt cgc ctt gca gaa gtc tgg atg gat gaa tac aag Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys			1344

435	440	445	
gaa ata ttt tat agg aga aat aca gat gca gca aaa att gtt aaa caa Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln 450	455	460	1392
aaa gca ttt ggt gat ctt tca aaa aga ttt gaa ata aaa cac cgt ctt Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu 465	470	475	1440
cgg tgt aaa aat ttt aca tgg tat ctg aac aac att tat cca gag gtg Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Asn Ile Tyr Pro Glu Val 485	490	495	1488
tat gtg cca gac ctt aat cct gtt ata tct gga tac att aaa agc gtt Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val 500	505	510	1536
ggt cag cct cta tgt ctg gat gtt gga gaa aac aat caa gga ggc aaa Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys 515	520	525	1584
cca tta att atg tat aca tgt cat gga ctt ggg gga aac cag tac ttt Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Asn Gln Tyr Phe 530	535	540	1632
gaa tac tct gct caa cat gaa att cgg cac aac atc cag aag gaa tta Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu 545	550	555	1680
tgt ctt cat gct caa ggt ctc gtt cag ctg aag gca tgt acc tac Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr 565	570	575	1728
aaa ggt cac aag aca gtt gtc act gga gag cag ata tgg gag atc cag Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln 580	585	590	1776
aag gat caa ctt cta tac aat cca ttc tta aaa atg tgc ctt tca gca Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala 595	600	605	1824
aat gga gag cat cca agt tta gtg tca tgc aac cca tca gat cca ctc Asn Gly Glu His Pro Ser Leu Val Ser Cys Asn Pro Ser Asp Pro Leu 610	615	620	1872
caa aaa tgg ata ctt agc caa aat gat taa gtgttcctta aaatataagtt Gln Lys Trp Ile Leu Ser Gln Asn Asp 625	630		1922
gaaaaaggaa atatttttc tcataaaaact gtgacttaggc atacactgta gtttttgaaa attatgcataa agcagctaaa tgtaacttat tccaaatgtca tttttcttat ttatatcttt atgttagcact actacagaaa ttctgcaagt ttctgtttca aagcacaata actagtaata ccaaagacta tttcaaaaatg tccagatgta gggaaagaga tgtttacagt atgatgaaaa taatttcca agtaaagtga tgtttgcgtg tttgtacac ttagggatat atatataatag			1982 2042 2102 2162 2222

ctacattcac acactcacaa tttaaaatat ttcccctagt tttttgggg gataggaaga	2282
aagatttgtt actgtatTTT tttaactaca taaaaataga tcaataaatg tcagcattgg	2342
cctctgtgta caaaccaaga gctttacag atccagaatt tattagttt aaatgcaggt	2402
gaacttttt ttgcgttgg tttacttgc tgtcaaATgt ttccCTAAAC atgaaactga	2462
ataaggagaa gagtatTTT aacactaaa ttcttggca aattttaaa catttttag	2522
tctgtataac actccacttg aagcacttaa gtcttcctta aatgacttt cttaagtaat	2582
gatactgtgt gtttcccaa agcactttt aaaaaatttt tataaattac tatctgttga	2642
aaaggtgtcc tttccTTTC ttctagtatt tttttctta ccaaaattca ctaatcttga	2702
atgtttgtga tattaaattt caaatgcaga atacttgact cattaaAGC taaattttgt	2762
tactgattca attataattt taatggattt ttgactttgt aatggattct tttcatcaaa	2822
aagccttattt atttttATC tatgtggaaa acacaataaa aaatcctcaa cactattgtt	2882
atcatttggtaaattt taagtgcTTA ttccTCTTTT gggtaaaATC tgtaatttgat aatagggtgg	2942
ggaaaaatgaa ttttgtatgc tgaatttcta agcgcctattt gttgtaaaaa ccatcagata	3002
tttcttatgg cacaAAAAAT gaggaatAGC aaaattcctg tgTTcaatat tttagaaaaatt	3062
ttgtattaaat ttctgataaa gttcCTtaag catctgatAG aatgatgttt taaaaaaatt	3122
tgacgcttgc ttaggagatt taccactttt ttttttgtt ttgcgtcatt ttatatttag	3182
atctcctgta ttcttGTTCC cgaagtaaaa tacgatcggt ttcatatttt aaatctggca	3242
gagcctcagc tgtacgaaaa agagcatata ctggTTattt accctatctt ctcattttttt	3302
gtttgttaat ttgaatttgtt attaaaaAGC ctgcattctg agctggacat ggtggctcag	3362
cttctaattcc cagcactttg gtaggcaaag gtgggaggat catttgagct caggagttcc	3422
agaccagcct gggcaacata gcaaaatctc atctctacaa aaagtaaaaaa ttAAAAAAATG	3482
aaattaaaaa taaaattacc taggtgtggt ggcacgcattc tgtagttcca gctatacagg	3542
aagggtgaggc agaagcattt gttgagcttgg gtagatcgag gctacagtga gctatgatta	3602
caccactgca ctTCAGTCTG tgtgactgag caagactctt tcaaaaaaaa aaaaaAGCCT	3662
acattctcca gttgattttt tccaactaat gtgtattatg tgcctaattt tctatcagaa	3722
gttgtattaa gcccgttttc acactgctgt taaagacata cctgagactg ggtaattttat	3782
aaagaaaaat agttcaatg gacccacagg tccgcgtggc tggggaaagct tcacaatcat	3842
ggcggaaaggt gaaagcatgt cttacgtgga ag	3874

<210> 52
 <211> 633
 <212> PRT

<213> human

<400> 52

Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
1 5 10 15

His Lys Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Ile Ile
20 25 30

Val Leu Val Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
35 40 45

Glu Ser Arg Met Glu Arg Asn Met Lys Asn Lys Asn Lys Met Leu Asp
50 55 60

Leu Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
65 70 75 80

Gln Ile Gly Ala Pro Val Arg Gln Asn Ile Asp Ala Gly Glu Arg Pro
85 90 95

Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Leu Asp
100 105 110

Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Ala Phe
115 120 125

Lys Thr Thr Asn Leu Ser Val Glu Glu Gln Lys Glu Lys Glu Arg Gly
130 135 140

Glu Ala Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
145 150 155 160

His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
165 170 175

Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
180 185 190

Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val
195 200 205

Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp
210 215 220

Asp Ala Ser Val Asp Glu Tyr Leu His Asp Lys Leu Asp Glu Tyr Val
225 230 235 240

Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Arg Glu Arg Lys Gly
245 250 255

Leu Ile Thr Ala Arg Leu Leu Gly Ala Thr Val Ala Thr Ala Glu Thr
260 265 270

Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu
275 280 285

Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro
290 295 300

Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser
305 310 315 320

Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser
325 330 335

Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp
340 345 350

Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser
355 360 365

Ile Ser Lys Glu Tyr Phe Glu Tyr Ile Gly Ser Tyr Asp Glu Glu Met
370 375 380

Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln
385 390 395 400

Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val
405 410 415

Phe Arg Ser Lys Ser Pro His Ser Phe Pro Lys Gly Thr Gln Val Ile
420 425 430

Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys
435 440 445

Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln
450 455 460

Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu
465 470 475 480

Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Asn Ile Tyr Pro Glu Val
485 490 495

Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val
500 505 510

Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys
515 520 525

Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe
530 535 540

Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu
545 550 555 560

Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr
565 570 575

Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln
580 585 590

Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala
595 600 605

Asn Gly Glu His Pro Ser Leu Val Ser Cys Asn Pro Ser Asp Pro Leu
610 615 620

Gln Lys Trp Ile Leu Ser Gln Asn Asp
625 630

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence Sequence

<220>

<223> chemically-synthesized oligonucleotide primer

<400> 53

ccgcacgaca accgcaccat

20

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 54
cgctccggcc cacaaatctc 20

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 55
ctccaatcgt ccctacagtc g 21

<210> 56
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 56
ccaagctatc acctcggcc 19

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 57
tgtttctgca atggtgaggt g 21

<210> 58
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 58
gcggctccaa gacttcctaa t 21

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 59
gctgccctaa agccaaactc t 21

<210> 60
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 60
agaggacagg gaggatcaag ttc 23

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 61
tggcgacact taccgagctt 20

<210> 62
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 62
ccatgccct ttagtagct gta 23

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 63
cttgactgtg gttactgctg atca 24

<210> 64
<211> 23
<212> DNA
<213> Artificial Sequence

<220>		
<223> chemically-synthesized oligonucleotide primer		
<400> 64		
gtatccaccg aatgtgaaaa cgt		23
<210> 65		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> chemically-synthesized oligonucleotide primer		
<400> 65		
tgtccctcgg aaaaactggt		20
<210> 66		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> chemically-synthesized oligonucleotide primer		
<400> 66		
agccaccgtt catggtctct		20
<210> 67		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> chemically-synthesized oligonucleotide primer		
<400> 67		
agaacggcac gcctacgat		19
<210> 68		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> chemically-synthesized oligonucleotide primer		
<400> 68		
aggttagcctt tgctgtactc atcat		25
<210> 69		
<211> 20		
<212> DNA		
<213> Artificial Sequence		

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 69
tcacacctgatt cttgcgtgct 20

<210> 70
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 70
ctgtgggtta ttatcaatct tttttctt 28

<210> 71
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 71
gcatgtacaa tggctgcgc 19

<210> 72
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 72
caagagctgt aaacggcgg 19

<210> 73
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 73
gagacaccat tgagacttga ccag 24

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 74
caccaagatg aagggttcggg 20

<210> 75
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 75
tgtgacagcc agctcgaaaa c 21

<210> 76
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 76
tggagagcca agactttcc a 21

<210> 77
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 77
gcctgccatt ctcagcaaa 19

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 78
acactgaatc cacccaggac a 21

<210> 79
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 79
caagtccttc cggcatgaa 19

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 80
ccaaaatcac ctttcctttg c 21

<210> 81
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 81
cttgacaaca cagcagcgac a 21

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 82
acttgaagat gtggaggccc a 21

<210> 83
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 83
tggtaagaa agcaccaatg c 21

<210> 84
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 84
ccacacacgc catctttctt c

21

<210> 85
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 85
ttgtctataa caccgcctt g

21

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 86
cggcgtggaa aataggagag t

21

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 87
aggagaagaa gctggcagga g

21

<210> 88
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 88
cttgatggcg ttggtgagc

19

<210> 89
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer
<400> 89
tgggtaccgt atgcctcga 19

<210> 90
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer
<400> 90
tgtattcaaa ggtgggccc 19

<210> 91
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer
<400> 91
tgctgggaca tgtaccgtca t 21

<210> 92
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer
<400> 92
ccagatgcgg tagccatca 19

<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer
<400> 93
gccttctctg tgcacggag 19

<210> 94
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 94
gtgagaccag cccaaagaca c 21

<210> 95
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 95
atgggagttg gtagggaccg 20

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 96
catgggaggg tgatccactt 20

<210> 97
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 97
ggctgcattg aaggcatgt 19

<210> 98
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 98
aaggcAAC tccacaggc 19

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 99
ttacccggaa gcgtatgtgc 20

<210> 100
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 100
gcctccctgg ttatttctcac c 21

<210> 101
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 101
gcggccgcac catgaggggc aaccactga tc 32

<210> 102
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 102
gcggccgcct agaaggcact gttccatga 29

<210> 103
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 103
gacgcgttgc ggccgcagca tggcggatac cggctt 36

<210> 104
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 104
aaaggatggc ggccgctcac tcgctgtcga atttga 36

<210> 105
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 105
gcggccgcag catggaccgc gcggggcgc 29

<210> 106
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 106
atgcatctag acagaaggcc ttggaggag 29

<210> 107
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 107
gcggccgcag gatgggatgc gtgaagtcca gg 32

<210> 108
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 108
gcggccgcac aaggctgctg ctggaaactgg ctctcagtgg ccgt 44

<210> 109
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 109
gcggccgcag aatggctcac cttaaggagac ta 32

<210> 110
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 110
gcggccgcctt attcattttg gctaaaaatc ca 32

<210> 111
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 111
cggagcatgg cggataccgg cttgcgcgc gtg 33

<210> 112
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 112
gwgcaagccg gtatccgcca t 21

<210> 113
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> chemically-synthesized oligonucleotide primer

<400> 113
auggcgaua ccggcuugcg c 21

<210> 114
<211> 21
<212> RNA
<213> Artificial Sequence

<220>

<223> chemically-synthesized oligonucleotide primer

<400> 114

gcgcaagccg guauccgc ca u

21